

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2003, 01:44:12 ; Search time 123 Seconds
(without alignments)
3050.209 Million cell updates/sec

Title: US-09-904-389-2
Perfect score: 4435
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Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2742.5	61.8	2890	5 PCT-US93-07347-1	Sequence 1, Appli
3	2742.5	61.8	3033	1 US-08-003-311B-1	Sequence 1, Appli
4	2742.5	61.8	3033	1 US-08-261-432-1	Sequence 1, Appli
5	2072	46.7	5890	1 US-07-928-464-3	Sequence 3, Appli
6	2072	46.7	5890	5 PCT-US93-07347-3	Sequence 3, Appli
7	2072	46.7	6312	1 US-08-003-311B-3	Sequence 3, Appli
8	2072	46.7	6312	1 US-08-261-432-3	Sequence 3, Appli
9	2069	46.7	6312	1 US-08-003-311B-7	Sequence 7, Appli
10	2069	46.7	6312	1 US-08-261-432-7	Sequence 7, Appli
11	2068	46.6	5890	1 US-07-928-464-6	Sequence 6, Appli
12	2068	46.6	5890	5 PCT-US93-07347-6	Sequence 6, Appli

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15	2063	46.5	5890	1 US-07-928-464-5	Sequence 5, Appli
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44	469.5	10.6	2510	2 US-08-888-982A-42	Sequence 42, Appli
45	469.5	10.6	2510	4 US-09-462-261-42	Sequence 42, Appli

ALIGNMENTS

RESULT 1
US-07-928-464-1
; Sequence 1, Application US/07928464
; Patent No. 5367065
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene and
; TITLE OF INVENTION: Mutations
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
; ADDRESSEE: No. 5367065ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/928,464
; FILING DATE: 19920810
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Suzanne E.
; REGISTRATION NUMBER: 32,279
; REFERENCE/DOCKET NUMBER: UPN-1086
; TELEPHONE: 215-568-3100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2890 base pairs

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; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 118..2583
CS-07-928-464-1

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Alignment Scores:		
Pred. No.:	2,82e-272	2890
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Best Local Similarity:	62.33%	144
Query Match:	61.84%	87
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	Matches:	
	Conservative:	
	Mismatches:	
	Indels:	
	Gaps:	

US-09-904-389-2 (1-850) X US-07-928-464-1 (1-2890)

QY	1	MetGluMetProGlyArgArgSerAspTyrSerLeuLeuSerGlnIleProAspGluGlu	20
DB	118	ATGGAATGCCCCGGTAGAAGATCTAATACACTTTGCTTAGTCAATTTTCTGACGATCAG	177
QY	21	ValGly-----ThrGlyAlaSerThrSerPheTyrAspSerValAlaAla-----	35
DB	178	GTGTCAGTTCCGTCACCGGAGCTCCTCCGCCTCACTATGATTCCTTGTGAGCGAAAAAC	237
QY	36	-----GlyGlyAsnValIleLysGlyArgThrAspArg--ValPheAsp	49
DB	238	AGGAGCAACCATACACGCGGAACACCGGAAAGCTAAGCGCGAGAGAGCGGATTTGAT	297
QY	50	TipAsp-----GlySerGlyAspHisArgLeuAsnThrGlnAlaTyrArgIle	65
DB	298	TGGGATCCTAGCGGTGGTGGTGGTGCATCATAGGTTGAATAATCAACCGAATCGGGTT	357
QY	66	Gly---AsnLeuTyr---SerTrpIleGlyLeuGlnArgHisSerSerGlySerSerTyr	83
DB	358	GGGAATAATATGATGCTTCGTCTCTAGGGTTGCAAGGCAATCCAGTGGGAGTAGTTTC	417
QY	84	AspAspSerSerLeuSerSerAspTyrTyrAlaProThrLeuSerAsnProAlaAlaAsn	103
DB	418	GGTGAGAGCTCTTGTCTGGGGATTATTACATGCCTACGCCTTCT--GCGGCGGGTAAC	474
QY	104	GluIleAsnAlaLeuGluTyrIleLeuAspAspAspPheArgVal-----	118
DB	475	GAGATCGAATCTCTGTGGATTTCCTCAAGATGATGGGTTTAGGCTTGGATTTCGTTGGTGGT	534
QY	119	-----MetLysAlaValGlySerGlyGly---SerSerGlyLys	130
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QY	131	SerTrpAlaGlnGlnThrGluGluSerPheGlnLeuGlnGlnProLeuValLeuArgLeu	150
DB	595	AGCTGGCGGCAGCAGACGGAGGAGATTATCAGCTGCAGCTTGCAATGGCGTTAAGGCTT	654
QY	151	SerSerAsp**ThrCysAlaAspAspProAsnPheMetAspProIleProAspGluAla	170
DB	655	TCGTGGAGGGTACTTGTGCGACGATCCGAACTTCTGGATCCTGTACCGGACGAGTCT	714
QY	171	AlaLeuArgSerLeuSerIleSerAlaGluAlaIleSerHisArgPheTrpValAsnGly	190
DB	715	GCCTTACGGACTTCGCCCAAGTTACGCCGAAACCGGTTTCACATCGTTTCTGGTTAATGCG	774
QY	191	CysMetSerTyrLeuGluLysValProAspGlyPheTyrLeuIleHisGlyMetAspPro	210
DB	775	TGCTTATCGTACTATGATAAAGTTCTCTGATGGGTTTATATGATGAATGTCCTGGATCCC	834
QY	211	TyrValTrpSerLeuCysThrAsnLeuGlnGluAspGlyArgIleProSerPheGluSer	230
DB	835	TATATTGGACCTTATGCATCGACCTGCATGAAAGTGGTCGCATCCCTTCAATTGAATCA	894
QY	231	LeuLysThrValAspSerSerIleGlySerSerIleGluValValLeuIleAspArgHis	250

QY 611 PheHisProGluArgValAsnGluPheLeuArgGluValAlaIleMetLysSerLeuArg 630
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Db 1870 TTCCATGCTGAGCGTGTAAATGAGTTCTTAAGAGAGGTTGCGATAATGAAACGCTTCGC 1929

QY 631 HisProAsnIleValLeuPheMetGlyAlaValThrLysProProAsnLeuSerIleVal 650
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Db 1930 CACCCTAACATTGTTCTTTCATGGGTGCGGTCACTCAACCTCCAAATTTGTCAATAGTG 1989

QY 651 ThrGluTyrLeuSerArgGlySerLeuTyrArgLeuLeuHisLysSerGlyValLysAsp 670
| | | | |
Db 1990 ACAGAAATATTGTCAGAGGTTAGTTTATACAGACTTTTGCATAAAAGTGGAGCAAGGGAG 2049

QY 671 ---IleAspGluThrArgArgIleAsnMetAlaPheAspValAlaLysGlyMetAsnTyr 689
| | | | |
Db 2050 CAATTAGATGAGAGACGTCGCTGAGTATGGCTTATGATGTGGCTAAGGGAATGAATTAT 2109

QY 690 LeuHisArgArgAspProIleValHisArgAspLeuLysSerProAsnLeuLeuVal 709
| | | | |
Db 2110 CTTCACAATCGCAATCCTCCAATTGTCATAGAGATCTAAATCTCCAAACTATTATTGGTT 2169

QY 710 AspLysLysTyrThrValLysValCysAspPheGlyLeuSerArgLeuLysAlaArgThr 729
| | | | |
Db 2170 GACAAAAAATATACAGTCAAGGTTTGATTTTGGTCTCTCGCGATTGAAGGCCAGCACG 2229

QY 730 PheLeuSerSerLysSerAlaAlaGlyThrProGluTyrMetAlaProGluValLeuArg 749
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Db 2230 TTTCTTTCTCGAAGTCAGCAGCTGGAACCCCGAGTGGATGGCACCAGAAAGTCTCGGA 2289

QY 750 AspGluProSerAsnGluLysSerAspValTyrSerPheGlyValIleLeuTrpGluLeu 769
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Db 2290 GATGAGCCGCTTAATGAAAGTCAGATGTGTACAGCTTCGGGTTCATCTTGTGGAGCTT 2349

QY 770 AlaThrLeuGlnGlnProTyrCysAsnLeuAsnProAlaGlnValValAlaAlaValGly 789
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QY 790 PheLysGlyLysArgLeuAspIleProArgAspValAsnProLysLeuAlaSerLeuIle 809
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QY 810 ValAlaCysTrpAlaAspGluProTyrLysArgProSerPheSerIleMetGluThr 829
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Db 2470 GAGGTTGTGGACCAATGAGCCATGGAAGCGTCCATCATTTGCAACTATAATGGAATTG 2529

QY 830 LeuLysProMetThrLysGlnAlaProProGlnGlnSerArgThrAsp 845
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RESULT 2

PCT-US93-07347-1
; Sequence 1, Application PC/TUS9307347
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene and
; TITLE OF INVENTION: Mutations
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
; ADDRESSEE: Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07347

; FILING DATE: 19930805
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Suzanne E.
; REGISTRATION NUMBER: 32,279
; REFERENCE/DOCKET NUMBER: UPN-1086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2890 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 118..2583
PCT-US93-07347-1

Alignment Scores:
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Score: 2742.50 Matches: 546
Percent Similarity: 73.63% Conservative: 99
Best Local Similarity: 62.33% Mismatches: 144
Query Match: 61.84% Indels: 87
DB: 5 Gaps: 14

US-09-904-389-2 (1-850) x PCT-US93-07347-1 (1-2890)

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QY 21 ValGly-----ThrGlyAlaSerThrSerPheTyrAspSerValAlaAla----- 35
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Db 178 GTGTCAGTTTCGTCACCGGAGCTCCTCCGCTCACTATGATTCCTTGTGAGCGAAAAAC 237

QY 36 -----GlyGlyAsnValIleLysGlyArgThrAspArg---ValPheAsp 49
| | | | |
Db 238 AGGAGCAACCAATAACAGCGGGAACACCGGGAAGCTAAGCGGAGAGAGCGGATTGAT 297

QY 50 TrpAsp-----GlySerGlyAspHisArgLeuAsnThrGlnAlaTyrArgIle 65
| | | | |
Db 298 TGGGATCCTAGCGGTGGTGGTGGTGATCATAGGTTGAATAATCAACCGAATCGGGTT 357

QY 66 Gly---AsnLeuTyr---SerTrpIleGlyLeuGlnArgHisSerSerGlySerSerTyr 83
| | | | |
Db 358 GGAATAATATGATGCTTCGTCTCTAGGTTGCAAGGCAATCCAGTGGGAGTAGTTTC 417

QY 84 AspAspSerSerLeuSerSerAspTyrTyrAlaProThrLeuSerAsnProAlaAlaAsn 103
| | | | |
Db 418 GGTGAGAGCTCTTGTCTGGGGATTATTACATGCCTACGCTTCT---GCGGCGGCTAAC 474

QY 104 GluIleAsnAlaLeuGluTyrIleLeuAspAspAspPheArgVal----- 118
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Db 475 GAGATCGAATCTGTGGATTTCCTCAAGATGATGGGTTTAGCTTGGATTGGTGGTGGT 534

QY 119 -----MetLysAlaValGlySerGlyGly---SerSerGlyLys 130
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Db 535 GGAGGAGATTGAGGATACAGATGGCGCGGACTCCGCTGGAGGGTCTTTCATCTGGGAAG 594

QY 131 SerTrpAlaGlnThrGluSerPheGlnLeuGlnGlnProLeuValLeuArgLeu 150
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Db 595 AGCTGGGCGCAGCAGCGGAGAGATTATCAGCTGCAGCTTCATTGGCGTTAAGGCTT 654

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Db 655 TCGTCGGAGGCTACTTGTGCCGACGATCCGAACTTTCTGGATCCTGTACCGGACGAGTCT 714

QY 171 AlaLeuArgSerLeuSerIleSerAlaGluAlaIleSerHisArgPheTrpValAsnGly 190
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Db 715 GCTTTACGGACTTCGCCAAGTTTCAGCGGAAACCGTTTTCATCGTTTCTGGGTTAATGGC 774

QY 191 CysMetSerTyrLeuGluLysValProAspGlyPheTyrLeuIleHisGlyMetAspPro 210
Db 775 TGCTATCGTACTATGATAAAAGTTCTGTGATGGTTTATATGATGAATGGTCTGGATCCC 834
QY 211 TyrValTyrSerLeuCysThrAsnLeuGlnGluAspGlyArgIleProSerPheGluSer 230
Db 835 TATATTGGACCTTATGCATCGACCTGCATGAAAAGTGGTCGCATCCCTTCAATTGAATCA 894
QY 231 LeuLysThrValAspSerIleGlySerIleGluValValLeuIleAspArgHis 250
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QY 251 SerAspAlaSerLeuLysGluLeuGlnAsnArgValHisAsnIleSerSerCysVal 270
Db 955 AGTGATCCAGCCTTCAAGAACTTCAAAATAGAGTCCACGACATATCTTGTAGCTGCATT 1014
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Db 1015 ACCACAAAGAGGTTGTTGATCAGCTGGCAAAGCTTATCTGCAATCGTATGGGGGTCCA 1074
QY 291 ValSerGluGlyGluAspLeuValSerAlaTyrLysGluCysSerAspLeuLys 310
Db 1075 GTTATCATGGGGGAAGATGAGTTGGTTCCCATGTGGAAGGAGTGCAATGATGGTCTAAAA 1134
QY 311 GluCysLeuGlySerAlaValIleProLeuCysSerLeuSerValGlyLeuCysArgHis 330
Db 1135 GAA--ATCTTTAAAGTGGTGGTTCCCATAGGTAGCCTCTCTGTTGGACTCTGCAGACAT 1191
QY 331 ArgAlaLeuLeuPheLysValLeuAlaAspSerIleAspLeuProCysArgIleAlaLys 350
Db 1192 CGAGCTTTACTCTTCAAAGTACTGGCTGACATAATTGATTACCTCTCGAATTGCCAAA 1251
QY 351 GlyCysLysTyrCysThrArgAspAspAlaSerSerCysLeuValArgPheGlyLeuAsp 370
Db 1252 GGATGTAAATATTGTAATAGAGACGATGCCGCTTCGTGCCTTGTACAGTTTGGCCTTGAT 1311
QY 371 ArgGluTyrLeuIleAspLeuIleGlyArgProGlyCysLeuCysGlnProAspSerLeu 390
Db 1312 AGGGAGTACCTGGTTGATTAGTAGGAAAGCCAGGTCACCTTATGGAGCCTGATTCCCTTG 1371
QY 391 LeuAsnGlyProSerSerIleSerIleSerSerProLeuArgPheProArgLeuLysPro 410
Db 1372 CTTAAATGGTCCCTTCATCTATCTCAATTTCTTCTCTCTGCGGTTTCCACGACCAAAGCCA 1431
QY 411 IleGluSerThrIleAspPheArgSerLeuAlaLysGlnTyrPheLeuAspSerGlnSer 430
Db 1432 GTTGAACCCGCGAGTCGATTTTAGGTTACTAGCCAAACAATATTTCTCCGATAGCCAGTCT 1491
QY 431 LeuAsnLeuValPheAspGluAlaSerSerGlyAsnValValSerGlyLysAspAlaAla 450
Db 1492 CTTAATCTTGTTTTCGATCTCTGCATCAGAT-----GATATGGGA 1530
QY 451 PheSerValTyrGlnArgProLeuAsnArgLysAspValAspGlyLysThrIleValVal 470
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QY 471 ThrGlyAspLysAspArgAsnSerGlnLeuLeuAsnLysLysAlaAlaGlnLeuAsnThr 490
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QY 491 GlnAspGlyLysSerGluGlnPheArgSerCysValAlaSerProTyrSerValGlnSer 510
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QY 511 ThrProPheValGluAsnValValProLeuSerHisIleSerHisIleGlySerGluAsp 530
Db 1606 TTGCCACCCAGTGTAAATATGCTCCA----- 1632
QY 531 SerGluHisLeuLeuAlaLeuSerHisProArgMetAspHisValAsnAsnLeuProPhe 550
Db 1633 ---CAGAACATGATGCGTGGTCAAAATCAAATTGAAGCAGCACCTATGAATGCCCA 1689

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Db 1690 ATCAGTCAGCCAGTTCCAAACAGGGCAATAATAGGAACTTTGGACTTGATGGTGATATG 1749
QY 571 ValIleProTyrThrAspLeuAspLeuArgGluLysIleGlyAlaGlySerPheGlyThr 590
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QY 671 ---IleAspGluThrArgArgIleAsnMetAlaPheAspValAlaLysGlyMetAsnTyr 689
Db 2050 CAATTAGATGAGAGACGTCGCCCTGAGTATGGCTTATGATGTGGCTAAGGAATGAATTAT 2109
QY 690 LeuHisArgArgAspProProIleValHisArgAspLeuLysSerProAsnLeuLeuVal 709
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Db 2170 GACAAAAAATATACAGTCAAGGTTTGTGATTTTGGTCTCTCGCGATTGAAGGCCAGCACG 2229
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QY 750 AspGluProSerAsnGluLysSerAspValTyrSerPheGlyValIleLeuTyrGluLeu 769
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Db 2410 TTCAAGTGTAAACGGCTGGAGATCCCGGTAATCTGAAATCTCAGGTTGCAGCCATAATC 2469
QY 810 ValAlaCysTyrAlaAspGluProTyrLysArgProSerPheSerSerIleMetGluThr 829
Db 2470 GAGGTTGTTGGACCAATGAGCCATGGAAAGCGTCCATCATTTGCAACTATAATGGACTTG 2529
QY 830 LeuLysProMetThrLysGlnAlaProProGlnSerArgThrAsp 845
Db 2530 CTAAGACCATTTGATCAAAATCAGCGGTTCTCTCCGCCCAACCGCTCGGAT 2577

RESULT 3

US-08-003-311B-1
; Sequence 1, Application US/08003311B
; Patent No. 5444166
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene
; TITLE OF INVENTION: and Mutations
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
; ADDRESSEE: No. 5444166ris

STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/003,311B
FILING DATE: January 12, 1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/928,464
FILING DATE: August 10, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: UPN-1108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3033 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 118..2583
US-08-003-311B-1

Alignment Scores:
Pred. No.: 3,06e-272 Length: 3033
Score: 2742.50 Matches: 546
Percent Similarity: 73.63% Conservative: 99
Best Local Similarity: 62.33% Mismatches: 144
Query Match: 61.84% Indels: 87
DB: 1 Gaps: 14

US-09-904-389-2 (1-850) x US-08-003-311B-1 (1-3033)

QY 1 MetGluMetProGlyArgArgSerAspTyrSerLeuLeuSerGlnIleProAspGluGlu 20
118 ATGGAATGCCGGTAGAAGATCTAATACACTTTCCTAGTCAATTTCTGACGATCAG 177	
QY 21 ValGly-----ThrGlyAlaSerThrSerPheTyrAspSerValAlaAla----- 35	
178 GTGTCAGTTTCGTCACCGGAGCTCCTCCGCCTCACTATGATCCTTGTGCGAGGAAAC 237	
QY 36 -----GlyGlyAsnValIleLysGlyArgThrAspArg---ValPheAsp 49	
238 AGGAGCAACCATAAACAGCGGGAACACCGGGAAGCTAAGCGGAGAGAGCGCGATTTGAT 297	
QY 50 TrpAsp-----GlySerGlyAspHisArgLeuAsnThrGlnAlaTyrArgIle 65	
298 TGGGATCCTAGCGGTGGTGGTGGTGATCATAGTTGAATAATCAACCGAATCGGGTT 357	
QY 66 Gly---AsnLeuTyr---SerTrpIleGlyLeuGlnArgHisSerSerGlySerSerTyr 83	
358 GGAATAATATGATGCTTCGTCTCTAGGGTTGCAAGGCAATCCAGTGGGAGTAGTTTC 417	
QY 84 AspAspSerSerLeuSerSerAspTyrTyrAlaProThrLeuSerAsnProAlaAlaAsn 103	
418 GGTGAGAGCTCTTTGCTGGGATTTATCATGCCTACGCTTCTCT---GCGGCGGCTAAC 474	
QY 104 GluIleAsnAlaLeuGluTyrIleLeuAspAspPheArgVal----- 118	
475 GAGATCGAATCTGTTGGATTTCCTCAAGATGATGGTTTAGGCTTGGATTGGTGGTGGT 534
Db

QY 119 -----MetLysAlaValGlySerGlyGly---SerSerGlyLys 130
535 GGAGGAGATTGAGGATACAGATGGCGGAGCTCCGCTGGAGGCTCTTCATCTGGGAAG 594	
QY 131 SerTrpAlaGlnGlnThrGluSerPheGlnLeuGlnGlnProLeuValLeuArgLeu 150	
595 AGCTGGGCGAGCAGACGAGGAGAGTATTATCAGCTGAGCTTGCAATGGCGTTAAGGCTT 654	
QY 151 SerSerAsp**ThrCysAlaAspAspProAsnPheMetAspProIleProAspGluAla 170	
655 TCGTCGGAGGCTACTTGTGCGGAGGATCCGAACCTTTCTGGATCCTGTACCGGAGGCTCT 714	
QY 171 AlaLeuArgSerLeuSerIleSerAlaGluAlaIleSerHisArgPheTrpValAsnGly 190	
715 GCTTTACGGACTTCGCCAAGTTTCAGCCGAAACCGTTTCACATCGTTTCTGGGTTAATGGC 774	
QY 191 CysMetSerTyrLeuGluLysValProAspGlyPheTyrLeuIleHisGlyMetAspPro 210	
775 TGCTTATCGTACTATGATAAGTTCCTGATGGGTTTATATGATGAATGGTCTGGATCCC 834	
QY 211 TyrValTrpSerLeuCysThrAsnLeuGlnGluAspGlyArgIleProSerPheGluSer 230	
835 TATATTGGACCTTATGCATCGACCTGCATGAAAGTGGTGGCATCCCTTCAATTGAATCA 894	
QY 231 LeuLysThrValAspSerSerIleGlySerSerIleGluValValLeuIleAspArgHis 250	
895 TTAAGAGCTGTTGATCTGCTGTTGATCTTCGCTTGAAGCGCATCATAGTTGATAGGCGT 954	
QY 251 SerAspAlaSerLeuLysGluLeuGlnAsnArgValHisAsnIleSerSerSerCysVal 270	
955 AGTGATCCAGCTTCAAGGAACCTTCACAATAGATGCCACGACATATCTTGTAGTGCATT 1014	
QY 271 ThrThrLysGluValAlaAspHisIleAlaLysLeuValCysAsnHisLeuGlyGlySer 290	
1015 ACCACAAAGAGGTTGTTGATCAGCTGGCAAGCTTATGCAATCGTATGGGGGGTCCA 1074	
QY 291 ValSerGluGlyGluAspLeuValSerAlaTrpLysGluCysSerAspAspLeuLys 310	
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QY 311 GluCysLeuGlySerAlaValIleProLeuCysSerLeuSerValGlyLeuCysArgHis 330	
1135 GAA---ATCTTTAAAGTGGTGGTTCCTCCATAGGTAGCTCTCTGTTGGACTCTGCAGACAT 1191	
QY 331 ArgAlaLeuLeuPheLysValLeuAlaAspSerIleAspLeuProCysArgIleAlaLys 350	
1192 CGAGCTTTACTCTTCAAAGTACTGGCTGACATAATTGATTTACCTGTGCAATTGCCAAA 1251	
QY 351 GlyCysLysTyrCysThrArgAspAlaSerSerCysLeuValArgPheGlyLeuAsp 370	
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QY 371 ArgGluTyrLeuIleAspLeuIleGlyArgProGlyCysLeuCysGlnProAspSerLeu 390	
1312 AGGAGTACCTGGTTGATTTAGTAGGAAGCCAGGTCACTTATGGGAGCCTGATTCCTTG 1371	
QY 391 LeuAsnGlyProSerSerIleSerIleSerSerProLeuArgPheProArgLeuLysPro 410	
1372 CTAAATGGTCTCTCATCTATCTCAATTTCTCTCTCTGCGGTTCCACGACCAAGCCA 1431	
QY 411 IleGluSerThrIleAspPheArgSerLeuAlaLysGlnTyrPheLeuAspSerGlnSer 430	
1432 GTTGAACCCGAGTCGATTTTAGGTTACTAGCCAAACAATAATTTCTCCGATAGCCAGTCT 1491	
QY 431 LeuAsnLeuValPheAspGluAlaSerSerGlyAsnValValSerGlyLysAspAlaAla 450	
1492 CTTAATCTTGTTCGATCTCTGCATCAGAT-----GATATGGGA 1530	
QY 451 PheSerValTyrGlnArgProLeuAsnArgLysAspValAspGlyLysThrIleValVal 470	
1531 TTCTCAATGTTTCATAGGCAATATGATAATATCCGGTGGAGAGAATGACGCATTGGCAGAA 1590
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QY 471 ThrGlyAspLysAspArgAsnSerGlnLeuLeuAsnLysLysAlaAlaGlnLeuAsnThr 490
Db 1591 AATGGTGGT-----1599
QY 491 GlnAspGlyLysSerGluGlnPheArgSerCysValAlaSerProTyrSerValGlnSer 510
Db 1600 -----GGGTCT 1605
QY 511 ThrProPheValGluAsnValProLeuSerHisIleSerHisIleGlySerGluAsp 530
Db 1606 TTGCCACCCAGTGCTAATATGCCTCCA-----1632
QY 531 SerGluHisLeuLeuAlaLeuSerHisProArgMetAspHisValAsnAsnLeuProPhe 550
Db 1633 ---CAGAACATGATGCGTGCCTCAAAATCAAAATGAAGCAGCACCTATGAATGCCACCA 1689
QY 551 ValHisGlySerGlnLeuIleArgLysProAsnGluLeuSerLeuGlyLeuGluAspLeu 570
Db 1690 ATCAGTCAGCCAGTCCAAACAGGGCAATAGGGAACCTTGACTTGATGGTGATGATG 1749
QY 571 ValIleProTyrThrAspLeuAspLeuArgGluLysIleGlyAlaGlySerPheGlyThr 590
Db 1750 GACATCCCGTGGTGATCTTAATAAAAGAAAAGATTGGAGCAGGTTCTTTGGCACT 1809
QY 591 ValTyrArgGlyGluTyrHisGlySerAspValAlaValLysIleLeuThrGluGlnAsp 610
Db 1810 GTCCACCGTGCTGAGTGGCATGGCTCGGATGTGTGTGAAATTTCTCATGGAGCAAGAC 1869
QY 611 PheHisProGluArgValAsnGluPheLeuArgGluValAlaIleMetLysSerLeuArg 630
Db 1870 TTCCATGCTGAGCGTGTAATGAGTTCTTAAGAGAGGTTGCGATAATGAACGCCCTTCGC 1929
QY 631 HisProAsnIleValLeuPheMetGlyAlaValThrLysProAsnLeuSerIleVal 650
Db 1930 CACCTAACATTGTTCTTCTTCATGGTGCGGTCACTCAACCTCCAAATTTGTCAATAGTG 1989
QY 651 ThrGluTyrLeuSerArgGlySerLeuTyrArgLeuLeuHisLysSerGlyValLysAsp 670
Db 1990 ACAGATATTGTCAAGAGGTAGTTTATACAGACTTTTGATAAAGTGGAGCAAGGAG 2049
QY 671 ---IleAspGluThrArgArgIleAsnMetAlaPheAspValAlaLysGlyMetAsnTyr 689
Db 2050 CAATTAGATGAGAGACGTCGCTGAGTATGGCTATGATGTGGCTAAGGAATGAATTAT 2109
QY 690 LeuHisArgArgAspProIleValHisArgAspLeuLysSerProAsnLeuVal 709
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QY 710 AspLysLysTyrThrValLysValCysAspPheGlyLeuSerArgLeuLysAlaArgThr 729
Db 2170 GACAAAATAATATACAGTCAAGGTTTGTGATTTTGGTCTCTCGGATTAAGGCCAGCACG 2229
QY 730 PheLeuSerSerLysSerAlaAlaGlyThrProGluTyrProMetAlaProGluValLeuArg 749
Db 2230 TTTCTTTCTCGAAGTCAGCAGCTGGAACCCCGAGTGGATGGCACCAGAGTCTCTGCGA 2289
QY 750 AspGluProSerAsnGluLysSerAspValTyrSerPheGlyValIleLeuTyrGluLeu 769
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QY 770 AlaThrLeuGlnGlnProTyrCysAsnLeuAsnProAlaGlnValValAlaAlaValGly 789
Db 2350 GCTACATTGCAACAACCATGGGTAACTTAAATCCGGCTCAGGTTGTAGTCTCGGTTGGT 2409
QY 790 PheLysGlyLysArgLeuAspIleProArgAspValAsnProLysLeuAlaSerLeuIle 809
Db 2410 TTCAAGTGTAAACGGCTGGAGATCCCGCTAATCTGAATCTCTCAGGTTGCGAGCATAATC 2469
QY 810 ValAlaCysTrpAlaAspGluProTyrLysArgProSerPheSerSerIleMetGluThr 829
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QY 830 LeuLysProMetThrLysGlnAlaProProGlnGlnSerArgThrAsp 845

Db 2530 CTAAGACCATTCATCAAAATCAGCGTTCTCTCGGCCCAACCGCTCGGAT 2577
RESULT 4
US-08-261-432-1
; Sequence 1, Application US/08261432
; Patent No. 5602322
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene
; TITLE OF INVENTION: and Mutations
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
; ADDRESSEE: No. 5602322ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/261,432
; FILING DATE: June 17, 1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/003,311
; FILING DATE: January 12, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lori Y. Beardsell
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: UPN-1864
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3033 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 118..2583
; US-08-261-432-1
Alignment Scores:
Pred. No.: 3,06e-272 Length: 3033
Score: 2742.50 Matches: 546
Percent Similarity: 73.63% Conservative: 99
Best Local Similarity: 62.33% Mismatches: 144
Query Match: 61.84% Indels: 87
DB: 1 Gaps: 14
US-09-904-389-2 (1-850) x US-08-261-432-1 (1-3033)
QY 1 MetGluMetProGlyArgArgSerAspTyrSerLeuLeuSerGlnIleProAspGluGlu 20
Db 118 ATGGAATGCCCCGTAGAAGATCTAATTACACTTTGCTTAGTCAATTTCTGACGATCAG 177
QY 21 ValGly-----ThrGlyAlaSerThrSerPheTyrAspSerValAlaAala----- 35
Db 178 GTGTCAGTTTCCGTCCACCGGAGTCTCTCGCCTCCTCATATGATTCCTTGTGAGCGGAAAAC 237
QY 36 -----GlyGlyAsnValIleLysGlyArgThrAspArg---ValPheAsp 49
Db 238 AGGAGCAACCATAAACAGCGGGAACACCGGGAAGCTAAGCGGAGAGAGCGGATTTCAT 297

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QY 770 AlaThrLeuGlnGlnProTrrpCysAsnLeuAsnProAlaGlnValValAlaValGly 789
Db 2350 GCTACATTGCAACAACCATGGGTAACCTTAATCCGGTTCAGGTTGTAGCTGGGTTGGT 2409
QY 790 PheLysGlyLysArgLeuAspIleProArgAspValAsnProLysLeuAlaSerLeulle 809
Db 2410 TTCAAGTGTAAACGGCTGGAGATCCCGCTAATCTGAATCTCAGGTTGCAGGCATAATC 2469
QY 810 ValAlaCysTrpAlaAspGluProTrrpLysArgProSerPheSerSerileMetGluThr 829
Db 2470 GAGGTTGTTGGACCAATGAGCCATGGAAGCGTCCATCATTTGCAACTATATGGAATTG 2529
QY 830 LeuLysProMetThrLysGlnAlaProGlnGlnSerArgThrAsp 845
Db 2530 CTAAGACCATGATCAATCAGCGGTTCTCCGCCCAACCGCTCGGAT 2577

RESULT 5
US-07-928-464-3
; Sequence 3, Application US/07928464
; Patent No. 5367065
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene and
; TITLE OF INVENTION: Mutations
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
; ADDRESSEE: No. 5367065ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/928,464
; FILING DATE: 19920810
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Suzanne E.
; REGISTRATION NUMBER: 32,279
; REFERENCE/DOCKET NUMBER: UPN-1086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5890 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1..353
; FEATURE:
; NAME/KEY: exon
; LOCATION: 354..1001
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1002..1176
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1177..1477
; FEATURE:
; NAME/KEY: intron

; LOCATION: 1478..1574
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1575..1719
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1720..1936
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1937..2038
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2039..2173
; FEATURE:
; NAME/KEY: exon
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; FEATURE:
; NAME/KEY: intron
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; FEATURE:
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; NAME/KEY: exon
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; FEATURE:
; NAME/KEY: intron
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; NAME/KEY: exon
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; NAME/KEY: intron
; LOCATION: 3589..3668
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; NAME/KEY: exon
; LOCATION: 3669..3769
; FEATURE:
; NAME/KEY: intron
; LOCATION: 3770..3858
; FEATURE:
; NAME/KEY: exon
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; NAME/KEY: intron
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; NAME/KEY: exon
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; NAME/KEY: intron
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; NAME/KEY: exon
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; NAME/KEY: intron
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; NAME/KEY: exon
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; FEATURE:
; NAME/KEY: intron
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; FEATURE:
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; NAME/KEY: intron
; LOCATION: 4883..4959

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; FEATURE:
; NAME/KEY: exon
; LOCATION: 4950..5056
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; FEATURE:
; NAME/KEY: intron
; LOCATION: 5057..5890
US-07-928-464-3

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Alignment Scores:

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1.22e-202
Pred. No.:
Score: 2072.00
Percent Similarity: 41.83%
Best Local Similarity: 34.92%
Query Match: 46.72%
DB: 1
Length: 5890
Matches: 556
Conservative: 110
Mismatch: 159
Indels: 772
Gaps: 34

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US-09-904-389-2 (1-850) X US-07-928-464-3 (1-5890)

QY	1	MetGluMetProGlyArgArgSerAspTyrSerLeuLeuSerGlnIleProAspGluGlu	20
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QY	21	ValGly-----ThrGlyAlaSerThrSerPheTyrAspSerValAlaAala-----	35
DB	414	GTGTCAAGTTTCCGTCACCGGAGCTCCTCCGCCTCACTATGATTCCTTGTGCGAGCGAAAAC	473
QY	36	-----GlyGlyAsnValIleLysGlyArgThrAspArg--ValPheAsp	49
DB	474	AGGAGCAACCAATAACACGCGGAACACCGGGAAAGCTAAGCGGAGAGAGCGCGGATTGTAT	533
QY	50	TrpAsp-----GlySerGlyAspHisArgLeuAsnThrGlnAlaTyrArgIle	65
DB	534	TGGGATCCTAGCGGTGGTGGTGATCATAGGTTGAATAATCAACCGAATCGGGTT	593
QY	66	Gly---AsnLeuTyr---SerTrpIleGlyLeuGlnArgHisSerSerGlySerSerTyr	83
DB	594	GGGAATAATATGATGCTTCGTCTCTAGGGTTGCAAAAGCAATCCAGTGGAGTAGTTTC	653
QY	84	AspAspSerSerLeuSerSerAspTyrTyrAlaProThrLeuSerAsnProAlaAlaAsn	103
DB	654	GGTGAGAGCTCTTTGTCTGGGGATTATTACATGCTACGCTTTCT--GCGCGGCTAAC	710
QY	104	GluIleAsnAlaLeuGluTyrIleLeuAspAspAspPheArgVal-----	118
DB	711	GAGATCGAATCTGTTGGATTTCCTCAAGATGATGGGTTTAGGCTTGGATTGGTGGTGT	770
QY	119	-----MetLysAlaValGlySerGlyGly---SerSerGlyLys	130
DB	771	GGAGGAGATTGTAGGATACAGATGGCGCGGACTCCGCTGGAGGGTCTTCATCTCGGAAG	830
QY	131	SerTrpAlaGlnGlnThrGluGluSerPheGlnLeuGlnGlnProLeuValLeuArgLeu	150
DB	831	AGCTGGCGCCAGCAGACGGAGGAGATTATCAGCTGCAGCTTGCAATTGGCGTTAAGGCTT	890
QY	151	SerSerAsp***ThrCysAlaAspAspProAsnPheMetAspProIleProAspGluAla	170
DB	891	TCGTCGGAGGCTACTTGTGCCGACGATCCGAACCTTCTGGATCCTGTACCGGACGAGTCT	950
QY	171	AlaLeuArgSerLeuSerTleSerAlaGluAlaIleSerHisArgPheTrp-----	187
DB	951	GCTTTACGGACTTCGCCAAGTTCAGCCGAAACCGTTTCACATCGTTTCTGGGTAATTGTT	1010
QY	187	-----	187
DB	1011	CCTGTTAAGCTTTGTTTCCCAAAATATTGAATCGTGGTTATAGAGATATGGTCCCTCTTG	1070
QY	187	-----	187
DB	1071	TTTCCGAAGTTTCAGTTAGATCTCCTTACC AAAAGTCTATTATAGTAGCAATGAGATATGT	1130
QY	188	-----ValAsnGlyCysMe	192
DB	1131	TGTTTAGATACATTGCAGAGTATGANTGTTTGTGTGCTGCATCAGGTTTAATGGCTGCTT	1190

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Db	1191	ATCGTACTATGATAAAGTTCCCTGATGGGTTTTATATGATGAATGGTCTGGATCCCTATAT	1250
QY	212	lTrpSerLeuCysThrAsnLeuGlnGluAspGlyArgIleProSerPheGluSerLeuLy	232
Db	1251	TTGGACCTTATGCATCGACCTGCATGAAAAGTGGTCCGATCCCTTCAATTGAATCATTAAG	1310
QY	232	sThrValAspSerSerIleGlySerSerIleGluValValLeuIleAspArgHisSerAs	252
Db	1311	AGCTGTGTGATTCTGGTGTGATTCTTCGCTTGAAGCGCATCATAGTTGATAGCGGTAGTGA	1370
QY	252	pAlaSerLeuLysGluLeuGlnAsnArgValHisAsnIleSerSerSerCysValThrTh	272
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QY	272	rLysGluValAlaAspHisIleAlaLysLeuValCysAsnHisLeuGly	288
Db	1431	AAAAGAGTTGTGATCAGCTGGCAAAGCTTATCTGCAATCGTATCGGGTTTGTACTCAT	1490
QY	288	-----	288
Db	1491	ACAATCCTTACTATCCCTTTTGAACCTTATATTTTATATCTTCCCTGATTTCTCACATTG	1550
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Db	1611	CCATGTGGAAGAGTGCATTGATGGTCTAAAGAA--ATCTTTAAAGTGGTGGTTTCCCA	1667
QY	320	euCysSerLeuSerValGlyLeuCysArgHisArgAlaLeuLeuPhe-Lys	336
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QY	336	-----	336
Db	1728	AACTTTGTATGCTATCCCATGACATTTTAAGACATCTTGTGAATGATCATATAAATTATT	1787
QY	336	-----	336
Db	1788	GTGCTTCATCCATTGTGTTTTTATTGGAATACATATGAAGAACGTTGAATGTGAAAAAGTGG	1847
QY	336	-----	336
Db	1848	TGTTATTGATTAGAAAAAATAGGTTACTGATAGTTGAATGTTCCAAAGAAAAAAGTAT	1907
QY	337	-----ValleuAlaAspSerIleAspLeuProCysArg	347
Db	1908	TTTATATCTTCTATTGTTGGTGCATGCAGGTACTGGCTGACATAATTGATTTACCTGTCCGA	1967
QY	348	IleAlaLysGlyCysLysTyrCysThrArgAspAspAlaSerSerCysLeuValArgPhe	367
Db	1968	ATTGCCAAAGGATGTAAATATTGTAATAGAGACGATGCCGCTTCGTGCCCTTGTACAGTTT	2027
QY	368	GlyLeuAsp	370
Db	2028	GGGCTTGATAGGTATGATACAAGTGATTGCCGAAAGAGCCTTTATTTTCCCTATTTCTTTTG	2087
QY	370	-----	370
Db	2088	CTTTTGTGTTCTGGAAAAACAATTATAGCTCCAAATGTTTTCGCAGAAATATTAGGTTGATG	2147
QY	371	-----ArgGluTyrLeuIleAspLeuIleGlyArgProGly	382
Db	2148	ACGTGGAAAAATTTGTTTTTGGTTTTTCAGGGAGTACCTGGTTGATTTAGTAGGAAAGCCAGGT	2207
QY	383	CysLeuCysGlnProAspSerLeuLeuAsnGlyProSerSerIleSerIleSerSerPro	402
Db	2208	CACCTATGGAGCCCTGATTCCTTGTCTAAATGGTCCTTCACTCTATCTCAATTTCTTCTCT	2267

QY	403	LeuArgpPheProArgLeuLysProIleGluSerThrIleAspPheArgSerLeuAlaLys	422
Db	2268	CTGCGGTTTCCACGACCAAGCCAGTTGAACCCGCGAGTCGATTTTAGGTTACTAGCCAAA	2327
QY	423	GlnTyrPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAlaSer	439
Db	2328	CAATAATTCTCCGATAGCCAGTCTCTTAATCTTGTGTTTCGATCCTGCATCAGGTATCCC	2387
QY	439	-----	439
Db	2388	ATACAAAAAACCTGAATAATAATGTTAACTTTTGTGATGCTGCTTACATCTCGTTTGTGAT	2447
QY	440	-----SerGlyAsnValValSerGlyLysAspAlaAlaPheSerValTyrGlnArg	456
Db	2448	TTCCCTCTAAAAGAGTAATCTCCTATCA-----TTAGGGTATTT	2486
QY	457	ProLeuAsnArgLysAspValAspGlyLysThrIleVal	469
Db	2487	---CTTGATCATGCTCAGTATCTGAACTGTTAGTAGTCTTAGAATGATTCTATTGTTG	2543
QY	470	-----ValThrGlyAsp-----	473
Db	2544	TTTTCTTGTCTCTTTTCACTTTAGTTGTTTGGCTGTTGATGATGTTGTTTGTGTTGGTGG	2603
QY	474	-----LysAspArgAsnSerGlnLeuLeuAsnLysLysAlaAla	486
Db	2604	GTTCTTTGCCCTAAATGATATTTAAGGTTAACTGTTAGTCTGCTGTTCAAG-----	2654
QY	487	GlnLeuAsnThrGlnAspGlyLysSerGluGlnPheArgSerCysValAlaSerPro-Ty	506
Db	2655	-----CTTATGAATTCTAGTGCAATTATGTGCAAGACTTGTCTCTGGACTCTAAT	2705
QY	506	rSerVal-----GlnSerThrProPheValG1	515
Db	2706	TTCTTATATCTGCTGTTGTTGAATGGTTGTAGATGATATGGGATTTCTCAATGTTTCATAGG	2765
QY	515	uAsn---ValValProLeuSerHisIleSerHisIleGlySerGluAspSerGluHisLe	534
Db	2766	CAATATGATAATCCGGTGGAGAGAATGACGCAATGG-----CAGAAAATGGT	2813
QY	534	uLeuAlaLeuSerHisProArgMet-----	542
Db	2814	GGTGGTCTTTTGCCACCAGTCTTAATAATGCTCCACAGAACATGATGCGTGGCTCAAAT	2873
QY	543	-----AspHisValAsnAsnLeuProPheValHisGlySerGlnLeuIleArgLy	559
Db	2874	CAAAATTGAAGCAGCACCTATG-AAATGCCCCACCAATCAGTCAGCCAGTTCCAAAACAGGGC	2932
QY	559	sProAsnGluLeuSerLeuGlyLeuGluAspLeuValIleProTyrThrAspLeuAspLe	579
Db	2933	AAATAGGAACTTGGACTTGATGTTGATGATATGGACATCCCGTGGTGTGATCTTAATAT	2992
QY	579	uArgGluLysIleGlyAla-----	585
Db	2993	AAAAGAAAAGATTGGAGCAGGTAATAATTTTACGGAATAATAATGATTCGGTCTAAAAA	3052
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QY	585	-----	585
Db	3113	AATAAGGAAAAAGTGCCACCCATTTTGAGATTACATTCTTCTCTGTTGCCITTAATCTT	3172
QY	586	-----GlySerPheGlyThrValTyrArgGlyGluT	596
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QY	596	rpHisGlySer-----	599
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QY	599	-----	599

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QY	600	-----	-----AspValAlaValL	604	
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QY	604	ysIleLeuThrGluGlnAsp	PheHisProGluArgValAsnGluPheLeuArgGluVal-	623	
Db	3533	AAATTCATGAGCAAGACT	TTCCATGCTGAGCGTGTAAATGAGTCTTAAGAGAGGT-G	3591	
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QY	655	-----	-----	655	
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QY	667	lyValLysAsp---	IleAspGluThrArgArgIleAsnMetAlaPheAspVal-----	683	
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Db	3951	TAACTCCTTATGTTAC	ATGATGGGTGATTACTTCTCGATCTTGGTGTCTTCTTCACATGG	4010	
QY	684	-----	-----AlaLysGlyMetAsnTyrLeuHisArgArgAsp	694	
Db	4011	AACTTTCTTTCCAAT	TTCTCTGTACAGGCTAAGGGAATGAATATCTTTCACAATCGCAAT	4070	
QY	695	ProProfileValHisArg	AspLeuLysSerProAsnLeuLeuValAspLysLysTyrThr	714	
Db	4071	CCTCCAATTGTGCATAG	ATCTAAAATCTCCAAACTTATGTGTGACAAAAAATATACA	4130	
QY	715	ValLysVal--	-----	717	
Db	4131	GTCAAGGT-TTGA	ATCTAAATTAGAAATTTGTGTCCAAATGTTTGTATTTTGATATTTT	4199	
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Db	4190	ATTCCCTCTGTGAGACA	AGCTTATATATAAAATATGATTTTTTAATCTAAATTTGGTTGG	4249	
QY	717	-----	-----	717	
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QY	717	-----	-----	717	
Db	4310	CGTCTTAAAAACAAT	CAGAACATTAATATTCTAACTCCTCAATTTTGTCTTGAAATTTTCAG	4360	
QY	718	---CysAspPheGlyLeu	SerArgLeuLysAlaArgThrPheLeuSerLysSerAla	736	

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QY 737 AlaGlyThr----- 739
Dbb 4430 GCTGGAACCGTAAGTTTCAGTTTGTGTTTGAAGAACTAAACACGCTGAACAACGTAACCTTTCTT 4489
QY 740 -----ProGluTr 742
Dbb 4490 CTAGGTCTATTTTCCAATGAAGAACTAAATAATTACTGACTTTTGATATATCATCAGCCCGAGTG 4549
QY 742 pMetAlaProGluValLeuArgAspGluProSerAsnGluLysSerAspValTyrSerPh 762
Dbb 4550 GATGGCACCAAGTCTCTCGAGATGAGCCGCTCTAATGAAAAAGTCAGATGTGTACAGCTT 4609
QY 762 eGlyValIleLeuTrpGluLeuAlaThrLeuGlnGlnProTrpCysAsnLeuAsnProAl 782
Dbb 4610 CGGGGTCTATCTTGTGGAGCTTGCTACATTGCAACAACCATGGGGTAACCTAAATCCGGC 4669
QY 782 aGln----- 783
Dbb 4670 TCAGGTACTTCCCACTCTAAACATCCCAATAATAATGATATATTATTTGCACTTTGGAAGT 4729
QY 784 -----Va 784
Dbb 4730 CCTCACTCTACATTTTCATAACATGCTATATATGATCATCAACAATAATGTTCCATAGGT 4789
QY 784 lValAlaAlaValGlyPheLysGlyLysArgLeuAspIleProArgAspValAsnProLy 804
Dbb 4790 TGTAGCTGGGTGGTTTCAAGTGTAACGGCTGGAGATCCCGGTAATCTGAATCCTCA 4849
QY 804 sLeuAlaSerLeuIleValAlaCysTrpAla----- 814
Dbb 4850 GGTTCAGGCATAATCGAGGGTGTGTGGAC-CAAGTACGTTAAGATTTTCTATCTCTTT 4908
QY 815 -----AspGluProTr 818
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RESULT 6

PCT-US93-07347-3
; Sequence 3, Application PC/TUS9307347
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene and
; TITLE OF INVENTION: Mutations
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
; ADDRESSEE: Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07347
; FILING DATE: 19930805
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

; NAME: Miller, Suzanne E.
; REGISTRATION NUMBER: 32,279
; REFERENCE/DOCKET NUMBER: UPN-1086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5890 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1..353
; FEATURE:
; NAME/KEY: exon
; LOCATION: 354..1001
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1002..1176
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1177..1477
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1478..1574
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1575..1719
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1720..1936
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1937..2038
; FEATURE:
; NAME/KEY: intron
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; NAME/KEY: exon
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; LOCATION: 3203..3243
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; FEATURE:
; NAME/KEY: intron
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; FEATURE:
; NAME/KEY: exon
; LOCATION: 3859..3943
; FEATURE:

NAME/KEY:	intron	1.22e-202	Length:	5890
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FEATURE:	exon	41.83%	Conservative:	110
NAME/KEY:	4038..4136	34.92%	Mismatches:	159
LOCATION:	4038..4136	46.72%	Indels:	772
FEATURE:	intron	5	Gaps:	34
NAME/KEY:	4137..4369	PCT-US93-07347-3	US-09-904-389-2 (1-850) x PCT-US93-07347-3 (1-5890)	
LOCATION:	4137..4369			
FEATURE:	exon			
NAME/KEY:	4370..4438			
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NAME/KEY:	4439..4541			
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FEATURE:	exon			
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LOCATION:	4542..4673			
FEATURE:	intron			
NAME/KEY:	4674..4787			
LOCATION:	4674..4787			
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NAME/KEY:	4788..4882			
LOCATION:	4788..4882			
FEATURE:	intron			
NAME/KEY:	4883..4959			
LOCATION:	4883..4959			
FEATURE:	exon			
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LOCATION:	4960..5056			
FEATURE:	intron			
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LOCATION:	5057..5890			
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PCT-US93-07347-3				
Alignment Scores:				
Pred. No.:	1.22e-202	Length:	5890	
Score:	2072.00	Matches:	556	
Percent Similarity:	41.83%	Conservative:	110	
Best Local Similarity:	34.92%	Mismatches:	159	
Query Match:	46.72%	Indels:	772	
DB:	5	Gaps:	34	
US-09-904-389-2 (1-850) x PCT-US93-07347-3 (1-5890)				
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Qy	21	ValGly-----ThrGlyAlaSerThrSerPheTyrAspSerValAlaAla	35	
Db	414	GTGTCAGTTTCCGTCACCGGAGCTCCTCGCCTCACTATGATTCCTTGTGCGAGCGAAAAC	473	
Qy	36	-----GlyGlyAsnValIleLysGlyArgThrAspArg----ValPheAsp	49	
Db	474	AGGAGCAACCATAAACAGCGGGAACACCGGGAAAGCTAAGCGGAGAGAGCGCGATTGAT	533	
Qy	50	TrpAsp-----GlySerGlyAspHisArgLeuAsnThrGlnAlaTyrArgIle	65	
Db	534	TGGGATCCTAGCGGT		

Db 1848 TGTTATTGATTAGAAAAAATAGGTTACTGATAGTTGAATGTTCCAAAAGAAAAAGTAT 1907
QY 337 -----ValLeuAlaAspSerIleAspLeuProCysArg 347
Db 1908 TTTATATCTTCTATTGTTGTCATGCAGGTACTGGCTGACATAATGATTTACCTGTGCGA 1967
QY 348 IleAlaLysGlyCysLysTyrCysThrArgAspAlaSerSerCysLeuValArgPhe 367
Db 1968 ATTGCCAAAGGATGTAATAATATTGTAATAGACGATGCCGCTTCGTGCCCTTGTACAGGTTT 2027
QY 368 GlyLeuAsp----- 370
Db 2028 GGGCTTAGTAGGTATGATACAAAGTGATTGCCGAAAGAGCCCTTTATTTTCCTATTTTCTTTG 2087
QY 370 ----- 370
Db 2088 CTTTTTGTCTTGGAACAAATATAGCTCCAAATGTTTCGCAGAAATATTAGTTTGATG 2147
QY 371 -----ArgGluTyrIleuIleAspLeuIleGlyArgProGly 382
Db 2148 ACGTGGAAAAATTTGTTTTGTTTCAGGGAGTACCTGGTTGATTTAGTAGGAAAGCCAGGT 2207
QY 383 CysLeuCysGlnProAspSerLeuLeuAsnGlyProSerSerIleSerIleSerSerPro 402
Db 2208 CACTTATGGGAGCCTGATTCCTTGCTAAATGGTCCTTCATCTATCTCAATTTCTTCTCCT 2267
QY 403 LeuArgPheProArgLeuLysProIleGluSerThrIleAspPheArgSerLeuAlaLys 422
Db 2268 CTGCGGTTTCCACGACCAAGCCAGTTGAACCCGCGAGTCGATTTTAGGTACTAGCCAAA 2327
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Db 2448 TTCCCCPAAAAAGAGTAATCTCCATCA-----TTTAGGGTATT----- 2486
QY 457 ProLeuAsnArgLysAspValAspGlyLysThrIleVal----- 469
Db 2487 ---CTTGATCATGCTCAGTATCTGAAGTGTGTAGTCTTAGAATGATCTATTGTTG 2543
QY 470 -----ValThrGlyAsp----- 473
Db 2544 TTTTCTTGCTCTTTTTCACCTTTAGTTGTTTTCGCTGTGTATGTTGTTGGTGG 2603
QY 474 -----LysAspArgAsnSerGlnLeuLeuAsnLysLysAlaAla 486
Db 2604 GTTCTTTGCCTAATGATATTTAAGGTTAACTTGTGTAGTCTGCTGTTCAAG----- 2654
QY 487 GlnLeuAsnThrGlnAspGlyLysSerGluGlnPheArgSerCysValAlaSerPro-Ty 506
Db 2655 -----CTTATGAATTTCTAGTGCATTTATGTGCAAGACTTGTCTTCTGCACTCTAAT 2705
QY 506 rSerVal-----GlnSerThrProPheValG1 515
Db 2706 TTCTTATATCTGCTTGTGTTGAATGGTTGTAGATGATATGGGATTTCTCAATGTTTCATAGG 2765
QY 515 uAsn---ValValProLeuSerHisIleSerHisIleGlySerGluAspSerGluHisLe 534
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QY 534 uLeuAlaLeuSerHisProArgMet----- 542
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QY 585 ----- 585
Db 3053 TGCAAGAAATAATGAAATTTCTTGAGGAAGTGGTTTTGCTTTGGACTCTGTCTCTCGAACAA 3112
QY 585 ----- 585
Db 3113 AATAAGGAAAAAGTGCCACCCATTTTGAGATTACATTTCTCTGTGTCCTTTAAATTTCTT 3172
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Db 3173 CCACCTCTAATTTGAGCGACTGCTCTTTTCAGGTTTCCTTTGGCACTGTCCACCGTGTGAGT 3232
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QY 599 ----- 599
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QY 623 ----- 623
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Db 3652 TCTTGATTCCGCTGTCAGGTTGCGATAATGAACCGCTTCGCCACCCCTAACATTTGTTCTCT 3711
QY 637 heMetGlyAlaValThrLysProProAsnLeuSerIleValThrGluTyrLeuSer---- 655
Db 3712 TCATGGGTGCGTCACTCAACCTCCAAATTTGTCAATAGTGACAGAAATATTTGTC-AAGG 3770
QY 655 ----- 655
Db 3771 TACAATTAATTGGATTGGAAGGTTTGATGTACTGAGTGTAGAAATTTTGGCCTATAATGA 3830
QY 656 -----ArgGlySerLeuTyrArgLeuLeuHisLysSerG 667
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QY 683 ----- 683
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QY 717 ----- 717
Db 4190 ATTCTCTTGTGAGACAAGCTTATATATAAATTATGATTTTAAATCTTAAATGGTTTGG 4249
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QY 717 ----- 717
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Db 4670 TCAGGTACTTCCCACTCTAAACATCCCAATAATAATGATATATTATTTGCATTTGGAAGT 4729
QY 784 -----Va 784
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QY 784 lValAlaAlaValGlyPheLysGlyLysArgLeuAspIleProArgAspValAsnProLy 804
Db 4790 TGTAGCTGCGTTGGTTTCAAGTGTAACGGCTGGAGATCCCGCGTAATCTGAATCCTCA 4849
QY 804 sLeuAlaSerLeuIleValAlaCysTrpAla----- 814
Db 4850 GGTTCAGCCATAATCGAGGGTTGTGGAC-CAAGTACGTTAAGATTTTCTATCTCTTTT 4908
QY 815 -----AspGluProTr 818
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QY 818 pLysArgProSerPheSerIleMetGluThrLeuLysProMetThrLysGlnAlaPr 838
Db 4969 GAAGCGTCCATCATTTGCAACTATATATGACTTGCTAAGACCATTTGATCAATCAGCGGT 5028
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Db 5029 TCCTCCGCCCAACCGCTCGGAT 5050
RESULT 7
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US-08-003-311B-3
: Sequence 3, Application US/08003311B
: Patent No. 5444166
: GENERAL INFORMATION:
: APPLICANT: Ecker, Joseph R.
: APPLICANT: Kieber, Joseph J.
: TITLE OF INVENTION: Constitutive Triple Response Gene
: TITLE OF INVENTION: and Mutations
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
: ADDRESSEE: No. 544166ris
: STREET: One Liberty Place - 46th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: U.S.A.
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WordPerfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/003,311B
: FILING DATE: January 12, 1993
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/928,464
: FILING DATE: August 10, 1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Lori Y. Beardsell
: REGISTRATION NUMBER: 34,293
: REFERENCE/DOCKET NUMBER: UPN-1108
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 215-568-3100
: TELEFAX: 215-568-3439
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6312 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-003-311B-3

Alignment Scores:
Pred. No.: 1.37e-202 Length: 6312
Score: 2072.00 Matches: 556
Percent Similarity: 41.83% Conservative: 110
Best Local Similarity: 34.92% Mismatches: 159
Query Match: 46.72% Indels: 772
DB: 1 Gaps: 34

US-09-904-389-2 (1-850) x US-08-003-311B-3 (1-6312)
QY 1 MetGluMetProGlyArgArgSerAspTyrSerLeuLeuSerGlnIleProaspGluGlu 20
Db 776 ATGGAATGCGCGGTAGAGATCTAATACACTTTTGTAGTCAATTTTCTGACGATCAG 835
QY 21 ValGly-----ThrGlyAlaSerThrSerPheTyrAspSerValAlaAla----- 35
Db 836 GTGTCAGTTTCCTCACCGGAGCTCTCCGCCTCCTATGATTCCTTGTGAGCGCAAAAC 895
QY 36 -----GlyGlyAsnValIleLysGlyArgThrAspArg---ValPheAsp 49
Db 896 AGGAGCAACCAACAGCGGGGAACACCGGGAAGCTAAGCGGAGAGAGCGGGATTTGAT 955
QY 50 TrpAsp-----GlySerGlyAspHisArgLeuAsnThrGlnAlaTyrArgIle 65
Db 956 TGGGATCCTAGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1015
QY 66 Gly---AsnLeuTyr---SerTrpIleGlyLeuGlnArgHisSerSerGlySerSerTyr 83
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Db 1016 GGGAAATAATATGATGCTTCGTTCTAGGGTTGCCAAGCAATCCAGTGGAGTAGTTTC 1075
QY 84 AspAspSerSerLeuSerSerAspTyrTyrAlaProThrLeuSerAsnProAlaAlaAsn 103
Db 1076 GGTGAGAGCTCTTTGTCTGGGATATATACATGCCCTACGCTTTCT--CGCGCGGCTAAC 1132
QY 104 GluIleAsnAlaLeuGluTyrIleLeuAspAspAspPheArgVal----- 118
Db 1133 GAGATCGAATCTGTTGGATTTCTCTCAAGATGATGGGTTTAGGCTTGGATTGGTGGTGGT 1192
QY 119 -----MetLysAlaValGlySerGlyGly---SerSerGlyLys 130
Db 1193 GGAGGAGATTGAGGATACAGATGGCGCGGACTCCCGTGGAGGGTCTTCATCTGGGAAG 1252
QY 131 SerTrpAlaGlnGlnThrGluGluSerPheGlnLeuGlnGlnProLeuValLeuArgLeu 150
Db 1253 AGCTGGCGCAGCAGACGGAGGAGATTATCAGCTGCAGCTTGCAATTGGCGTTAAGGCTT 1312
QY 151 SerSerAsp***ThrCysAlaAspAspProAsnPheMetAspProIleProAspGluAla 170
Db 1313 TCGTCGGAGGCTACTTGTGCCGACCATCCGAACCTTCTCGATCCTGTACCGGACGAGTCT 1372
QY 171 AlaLeuArgSerLeuSerIleSerAlaGluAlaIleSerHisArgPheTrp----- 187
Db 1373 GCTTTACGGACTTCGCCAAGTTCAGCCGAAACCGTTTCACATCGTTTCTGGGTATTGTT 1432
QY 187 ----- 187
Db 1433 CCTGTTAAGCTTTGTTTCCCAAAATATTGAATCGTGGTTATAGAGATATGTCCTCTTG 1492
QY 187 ----- 187
Db 1493 TTTCCGAAGTTTCAGTTAGATCTCCTTACCAAAAGTCTANTAGTAGCAAAATCAGATATGT 1552
QY 188 -----ValAsnGlyCysMe 192
Db 1553 TGTTTAGATACATGTCAGAGTATGATGTTTGTGTGTGTCATCAGGTTAATGGCTGCTT 1612
QY 192 tSerTyrLeuGluLysValProAspGlyPheTyrLeuIleHisGlyMetAspProTyrVa 212
Db 1613 ATCGTACTATGATAAAGTTTCTGATGGGTTTTATATGATGAATGGTCTGGATCCCTATAT 1672
QY 212 lTrpSerLeuCysThrAsnLeuGlnGluAspGlyArgIleProSerPheGluSerLeuLy 232
Db 1673 TTGGACCTTATGATCGACCTGCATGAAAGTGGTCGCATCCCTTCAATTGAATCATTAAG 1732
QY 232 sThrValAspSerIleGlySerSerIleGluValValLeuIleAspArgHisSerAs 252
Db 1733 AGCTGTTGATTCTGGTGTGATTCTTCGCTTGAAGCGATCATAGTTGATAGGCGTAGTGA 1792
QY 252 pAlaSerLeuLysGluLeuGlnAsnArgValHisAsnIleSerSerSerCysValThrTh 272
Db 1793 TCCAGCCTTCAGGAACCTTCACAATAGAGTCCACGACATATCTTGTAGCTGCATTACCAC 1852
QY 272 rLysGluValAlaAspHisIleAlaLysLeuValCysAsnHisLeuGly----- 288
Db 1853 AAAAGAGTTTGTGATCAGCTGGCAAGCTTATCTGCAATCGTATGGGGTTTGTACTCAT 1912
QY 288 ----- 288
Db 1913 ACAATCCTTACTATCCCTTTGAACATTATATTTTATATCTTCCTGTGATTTCTCACAATTG 1972
QY 289 -----GlySer-ValSerGluGlyGluAspAspLeuValS 300
Db 1973 TACTCGTTAATTCTGTCTTCCCGAGGGTCCAGTTATCATGGGGGAAGATGAGTTGGTTC 2032
QY 300 erAlaTrpLysGluCysSerAspAspLeuLysGluCysLeuGlySerAlaValIleProL 320
Db 2033 CCATGTGGAAGGAGTGCATTGATGGTCTAAAGAA--ATCTTTAAAGTGGTGGTTCCTCCA 2089
QY 320 euCysSerLeuSerValGlyLeuCysArgHisArgAlaLeuLeuPhe-Lys----- 336
Db 2090 TAGGTAGCCTCTCTGTGGACTCTGCAGACATCGAGCTTTACTTCTTCAAAGTGAGATCCC 2149

QY 336 ----- 336
Db 2150 AACTTTGATGCTATCCCCATGACATTTAAGACATCTTGTGAAATGATCATATAAATTATT 2209
QY 336 ----- 336
Db 2210 GTGCTTCATCCATTTGTTTTTATTGGAATACATATGAAGAACGTTGAATGTGAAAGAGTGG 2269
QY 336 ----- 336
Db 2270 TGTTATTGATTAGAAAAAATAGGTTACTGTATAGTTGAAATGTTCCAAAGAAAAAGTAT 2329
QY 337 -----ValLeuAlaAspSerIleAspLeuProCysArg 347
Db 2330 TTTATATCTTCTATTTGGTGCAATGAGGTTACTGGCTGACATAATTGATTTACCTGTGCGA 2389
QY 348 IleAlaLysGlyCysLysTyrCysThrArgAspAspAlaSerSerCysLeuValArgPhe 367
Db 2390 ATTGCCAAAGGATGTAATATTGTAATAGAGACGATGCCGCTTCGTGCTTGTCAAGTTT 2449
QY 368 GlyLeuAsp----- 370
Db 2450 GGGCTTGATAGGTATGATACAAGTGATTCGAAAGAGCCTTTATTTTCTATTTTCTTTG 2509
QY 370 ----- 370
Db 2510 CTTTTTGTCTCGAAAAACAATTATAGCTCCAAATGTTTCGCAGAATATTAGTTGATG 2569
QY 371 -----ArgGluTyrLeuIleAspLeuIleGlyArgProGly 382
Db 2570 ACGTGGAAAAATTTGTTTTCAGGGAGTACCTGGTTGATTTAGTAGGAAAGCCAGGT 2629
QY 383 CysLeuCysGlnProAspSerLeuLeuAsnGlyProSerSerIleSerIleSerSerPro 402
Db 2630 CACTTATGGGAGCTGATTCCTTGTCTAAATGGTCTTTCATCTATCTCAATTTCTTCTCCT 2689
QY 403 LeuArgPheProArgLeuLysProIleGluSerThrIleAspPheArgSerLeuAlaLys 422
Db 2690 CTGCGGTTTCCACGACCAAGCCAGTTGAACCCGAGTCGATTTAGGTTACTAGCCAAA 2749
QY 423 GlnTyrPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAlaSer----- 439
Db 2750 CAATATTTCTCCGATAGCCAGTCTCTTAATCTTGTTTTCGATCCTGCATCAGGATTCCC 2809
QY 439 ----- 439
Db 2810 ATACAAAAAACCTTAATAATATGTTTAACTTTTTCATCTGCTGCTTACATCTCGTTTTGTAT 2869
QY 440 -----SerGlyAsnValValSerGlyLysAspAlaAlaPheSerValTyrGlnArg 456
Db 2870 TTCCCTTAAAGAGTAACTCTCCTATCA-----TTTAGGTTATTT----- 2908
QY 457 ProLeuAsnArgLysAspValAspGlyLysThrIleVal----- 469
Db 2909 ---CTTGATCATGTCAGTATCTGAAGTGTAGTAGTCTTGAATGATTCTATTGTTG 2965
QY 470 -----ValThrGlyAsp----- 473
Db 2966 TTTTCTTGTCTCTTTTCACTTTTAGTTGTTTGGCTGTTGATGTTGTTGTTGTTGTTG 3025
QY 474 -----LysAspArgAsnSerGlnLeuLeuAsnLysLysAlaAla 486
Db 3026 GTTCTTTGCCTAATGATATTAAAGGTTAAACTTGTAGTCTGCTGTTCAAG----- 3076
QY 487 GlnLeuAsnThrGlnAspGlyLysSerGluGlnPheArgSerCysValAlaSerPro-Ty 506
Db 3077 -----CTTATGAATCTAGTGCATTTATGTGCAAGACTTGTCTTCTGGACTCTAAT 3127
QY 506 rSerVal-----GlnSerThrPropheValGI 515
Db 3128 TTCTTATATCTGCTTGTGTAATGGTTGTAGATGATATGGGATTCTCAATGTTTTCATAGG 3187

QY 289 -----GlySer-ValSerGluGlyGluAspAspLeuValS 300
Db 1973 TACTCGTTAAATCTTGCTTCCCCAGGGTCCAGTTATCATGGGGAAGATGAGTTGGTTC 2032
QY 300 erAlaTrpLysGluCysSerAspAspLeuLysGluCysLeuGlySerAlaValIleProL 320
Db 2033 CCATGTGGAAGGAGTGCAATTGATGGTCTAAAGAA--ATCTTTAAAGTGGTGGTCCCA 2089
QY 320 euCysSerLeuSerValGlyLeuCysArgHisArgAlaLeuLeuPhe-Lys----- 336
Db 2090 TAGGTAGCCTCTCTGTGGACTCTGCAGACATCGAGCTTTACTCTTCAAAGTGAGATCCC 2149
QY 336 ----- 336
Db 2150 AACTTTGATGCTATCCCCATGACATTTAAGACATCTTGTGAAATGATCATATAAATTATT 2209
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QY 336 ----- 336
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QY 337 -----ValLeuAlaAspSerIleAspLeuProCysArg 347
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QY 348 IleAlaLysGlyCysLysTyrCysThrArgAspAspAlaSerSerCysLeuValArgPhe 367
Db 2390 ATTGCCAAAGGATGTAATATTGTAATAGAGACGATGCCGCTTCGTGCCTTGTTCAGGTTT 2449
QY 368 GlyLeuAsp----- 370
Db 2450 GGGCTTGATAGGTATGATACAAAGTGATTGCCAAAGAGCCCTTTATTTCCTATTTCCTTG 2509
QY 370 ----- 370
Db 2510 CTTTTTGTCTCGGAAAAACAATTATAGCTCCAAATGTTTCGCAGAAATATTAGGTTGATG 2569
QY 371 -----ArgGluTyrLeuIleAspLeuIleGlyArgProGly 382
Db 2570 ACGTGGAAAAATTTGTTTTGGTTTTCAGGGAGTACCTGGTTGATTTAGTAGGAAAGCCAGGT 2629
QY 383 CysLeuCysGlnProAspSerLeuLeuAsnGlyProSerSerIleSerIleSerSerPro 402
Db 2630 CACTATGGGAGCCTGATTCCTTGCTAAATGGTCCTTCATCTCATCTCAATTTCTTCCT 2689
QY 403 LeuArgPheProArgLeuLysProIleGluSerThrIleAspPheArgSerLeuAlaLys 422
Db 2690 CTGCGGTTTCCACGACCAAGCCAGTTGAACCCCGAGTCGATTTTAGGTTACTAGCCAAA 2749
QY 423 GlnTyrPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAlaSer----- 439
Db 2750 CAATATTTCTCCGATAGCCAGTCTCTTAATCTTGTTTTCGATCCCTGCATCAGGTATTCCC 2809
QY 439 ----- 439
Db 2810 ATACAAAAAACCTAAATAATATGTTAACTTTTTGCATGCTGCTTACATCTCGTTTGTAT 2869
QY 440 -----SerGlyAsnValValSerGlyLysAspAlaAlaPheSerValTyrGlnArg 456
Db 2870 TTCCCCCTAAAGAGTAATCTCCTATCA-----TTTAGGTAATTT----- 2908
QY 457 ProLeuAsnArgLysAspValAspGlyLysThrIleVal----- 469
Db 2909 ---CTTGATCATGCTCTCAGTATCTGAAGTGTAGTAGTCTTAGAATGATTCATTGTTTG 2965
QY 470 -----ValThrGlyAsp----- 473
Db 2966 TTTTCTTGCTCTTTTCACTTTTAGTTGTTTTTGGCTGTGATGTGTATGTTGTTGGTGG 3025
QY 474 -----LysAspArgAsnSerGlnLeuLeuAsnLysLysAlaAla 486

Db 3026 GTTCTTTGCCCTAATGATATTTAAGGTTAAACTTGTTAGTCTGCTGTTCAAG----- 3076
QY 487 GlnLeuAsnThrGlnAspGlyLysSerGluGlnPheArgSerCysValAlaSerPro-Ty 506
Db 3077 -----CTTATGAATTTCTAGTGCATTTATGTGCAAGACTTGTCTTCTGGACTCTAAT 3127
QY 506 rSerVal-----GlnSerThrProPheValG1 515
Db 3128 TTCTTATATCTGCTTGTGTTGAATGGTTGTAGATGATATGGGATTTCTCAATGTTTCATAGG 3187
QY 515 uAsn---ValValProLeuSerHisIleSerHisIleGlySerGluAspSerGluHisLe 534
Db 3188 CAATATGATAATCCGGTGGAGAGAAATGACGCATTGG-----CAGAAAATGGT 3235
QY 534 uLeuAlaLeuSerHisProArgMet----- 542
Db 3236 GGTGGTCTTTTGCACCCAGTGTCTAATATGCCTCCACAGAACATGATCGTGCCTCAAT 3295
QY 543 -----AspHisValAsnAsnLeuProPheValHisGlySerGlnLeuIleArgLy 559
Db 3296 CAAATTGAAGCAGCACCTATG-AATGCCCCACCAATCAGTCAGCCAGTTCCTCCAAACAGGCG 3354
QY 559 sProAsnGluLeuSerLeuGlyLeuGluAspLeuValIleProThrThrAspLeuAspLe 579
Db 3355 AAATAGGGAACCTTGGACTTGATGGTGTATGATATGGACATCCCGTGGTGTATCTTAATAT 3414
QY 579 uArgGluLysIleGlyAla----- 585
Db 3415 AAAAGAAAGATTGGAGCAGGTAATAATTTACGGAAAAATTAATGATTCGGTCTAAAAA 3474
QY 585 ----- 585
Db 3475 TGCAAAAGAAATATGAAATTTCTTGAGGAAGTGGTTTTTGTCTTGGACTCTGTTCTCGAACAA 3534
QY 585 ----- 585
Db 3535 AATAAGGAAAAAGTGCCACCATTTTTGAGATTACATTTCTCTGTGTGCCCTTTAATTCIT 3594
QY 586 -----GlySerPheGlyThrValTyrArgGlyGluT 596
Db 3595 CCACCTCTAATTTAGCGACTGCTCTTTTCAGGTTCTTTGGCACTGTCCACCGTGTGAGT 3654
QY 596 rpHisGlySer----- 599
Db 3655 GGCATGGCTCGGTAAGAACTTTTGTGCAGAAATTACGCAGCTGAATTTTTTTTCGCTCT 3714
QY 599 ----- 599
Db 3715 AAAAAATTGGTTGTGACTTTTGGATCTGCTTGGTATTATAAAAGGCAAGATTATTGTATA 3774
QY 599 ----- 599
Db 3775 TGTGACTCTCCGTTCTGTGAGAAAATTAAACACGGACAAAAGGTGTCCCATTTTAGATGTA 3834
QY 599 ----- 599
Db 3835 TATGTGCTTTTATATCATAAATTTGTCTTCTCTGTGTTGAATTTTACAATTCATCTACTAGA 3894
QY 600 -----AspValAlaValL 604
Db 3895 AGAATTTCTAATTTTGATTATTGCAGTAATATTCTCTATCAATTTTCAGGATGTTGCTGTA 3954
QY 604 ysIleLeuThrGluGlnAspPheHisProGluArgValAsnGluPheLeuArgGluVal- 623
Db 3955 AAATTCTCATGGAGCAAGACTTCCATGCTGAGCGTGTAAATGAGTTCTTAAAGAGAGGT-G 4013
QY 623 ----- 623
Db 4014 CACAAATAAAATTTTCTCTTGATTTTGGTAATGAACCTGTTGTATTAAATGTCCTCAATGA 4073
QY 624 -----AlaIleMetLysSerLeuArgHisProAsnIleValLeup 637

Db 4074 TCTTGANTCGCTGTGAGTTGCGGATAATGAACCGCTTCGCCACCCCTAACATTGTTCTCT 4133
QY 637 heMetGlyAlaValThrLysProAsnLeuSerIleValThrGluTyrLeuSer----- 655
Db 4134 TCATGGGTGCGGTCACTCAACCTCCAAATTGTCATAATGACAGATAATTTGTC-AAGG 4192
QY 655 ----- 655
Db 4193 TACAATTACTTGGATTGGAAGGTTTGATGTACTAGTGTAGAAATTTTGGCCTATAATGA 4252
QY 656 -----ArgGlySerLeuTyrArgLeuLeuHisLysSerG 667
Db 4253 CTCTAATACCATGANTTCTTTCAAACAGAGGTAGTTATACAGACTTTTGCATAAAAGTG 4312
QY 667 lyValLysAsp---ileAspGluThrArgArgileAsnMetAlaPheAspVal----- 683
Db 4313 GAGCAAGGAGCAATTAGATGAGAGACGTCGCCCTGAGTATGGCTTATGATGTGTATGTT 4372
QY 683 ----- 683
Db 4373 TAACTCCTTATGTTACATGATATGGGTGATTACTTCCCTGATCTTGGTGTCTTTCACATGG 4432
QY 684 -----AlaLysGlyMetAsnTyrLeuHisArgArgAsp 694
Db 4433 AACTTTCTTTCCAATTCTCTGTACAGGCTAAGGGAATGAATTATCTTCACAATCGCAAT 4492
QY 695 ProProileValHisArgAspLeuLysSerProAsnLeuLeuValAspLysLysTyrThr 714
Db 4493 CCTCCAATTGTGCATAGATCTAAAAATCTCCAAACTATTGTTGACAAAAAATATACA 4552
QY 715 ValLysVal----- 717
Db 4553 GTCAAGGT-TTGAATCTAAATTAGAAAATTGTTGTGCCAATGTTTGTATTTTGATATTTT 4611
QY 717 ----- 717
Db 4612 ATTCTCTTGTGAGACAAGCTTATATATAAATTATGATTTTAAATCTAAATTGGTTTG 4671
QY 717 ----- 717
Db 4672 AGACATTACAAAAAGGCGTTAATCTGCTGAAACTTAAAGATACAGCAGCCTCAAGCTGT 4731
QY 717 ----- 717
Db 4732 CGTCTTAAACAACATCAGAACATTATTATTCTTAACCTCCTCAATTTGTCTTGAATTTTCAG 4791
QY 718 ---CysAspPheGlyLeuSerArgLeuLysAlaArgThrPheLeuSerSerLysSerAla 736
Db 4792 GTTTGTGATTTGGTCTCTCGCGATGAAGGCCAGCGTTCTTTCTCCTCGAAGTCAGCA 4851
QY 737 AlaGlyThr----- 739
Db 4852 GCTGGAACCGTAAGTTCAGTTTGTGTTGAAACTAAACACCGCTGAACAACGTAACCTTCTT 4911
QY 740 -----ProGluTyr 742
Db 4912 CTAGGTCCTATTTCCAATGGAAGCTAAATAATTACTGACTTTGATATATACGCCCGAGTG 4971
QY 742 pMetAlaProGluValLeuArgAspGluProSerAsnGluLysSerAspValTyrSerPh 762
Db 4972 GATGGCACCAGAAGTCCTCGAGATGAGCCGCTCTAATGAAAAGTCAGATGTGTACAGCTT 5031
QY 762 eGlyValIleLeuTrpGluLeuAlaThrLeuGlnGlnProTrpCysAsnLeuAsnProAl 782
Db 5032 CGGGGTCACTCTGTGGGAGCTTGCTACATTTGCAACCAACCATGGGGTAACTTAAATCCGGC 5091
QY 782 agln----- 783
Db 5092 TCAGGTACTTCCCACTCTAAACATCCCAAATAATAATGATATATTTTGTGATTGGAAGT 5151
QY 784 -----Va 784
Db 5152 CCTCACTCTACATTTCAATAACATGCTATATATATGATCATCCAAACAAAATGTTCCATAGGT 5211

QY 784 lValAlaAlaValGlyPheLysGlyLysArgLeuAspIleProArgAspValAsnProLy 804
Db 5212 TGTAGCTGCGGTTGGTTTCAAGTGTAAACGGCTGGAGATCCCGGTAATCTGAATCCTCA 5271
QY 804 sLeuAlaSerLeuIleValAlaCysTrpAla----- 814
Db 5272 GGTTCAGCCATAATCGAGGTTGTTGGAC-CAAGTACGTTAAGATTTTCTATCTCTTTT 5330
QY 815 -----AspGluProTr 818
Db 5331 TTGAATTCCTTTGAATAGACTTCATGTTTATGTAATGTTTTCATTACCAGTGAGCCATG 5390
QY 818 pLysArgProSerPheSerSerIleMetGluThrLeuLysProMetThrLysGlnAlaPr 838
Db 5391 GAAGCGTCCATCATTTGCAACTATAATGGACTTGCTAAGACCATTGATCAAAATCAGCGGT 5450
QY 838 oProGlnGlnSerArgThrAsp 845
Db 5451 TCCTCCGCCCAACCGCTCGGAT 5472
RESULT 9
US-08-003-311B-7
; Sequence 7, Application US/08003311B
; Patent No. 5444166
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene
; TITLE OF INVENTION: and Mutations
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
; ADDRESSEE: No. 5444166ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/003,311B
; FILING DATE: January 12, 1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/928,464
; FILING DATE: August 10, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lori Y. Beardell
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: UPN-1108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6312 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-003-311B-7

Alignment Scores:
Pred. No.: 2,79e-202 Length: 6312
Score: 2069.00 Matches: 556
Percent Similarity: 41.83% Conservative: 110
Best Local Similarity: 34.92% Mismatches: 159
Query Match: 46.65% Indels: 772

DB: 1 Gaps: 34

US-09-904-389-2 (1-850) x US-08-003-311B-7 (1-6312)

QY 1 MetGluMetProGlyArgArgSerAspTyrSerLeuLeuSerGlnIleProAspGluGlu 20
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776 ATGGAATGCCCGTAGAAGATCTAATTACACTTTGCTTAGTCAATTTTCTGACGATCAG 835

QY 21 ValGly-----ThrGlyAlaSerThrSerPheTyrAspSerValAlaAla----- 35
|||||
836 GTGTCAGTTTCCGTCACCGGAGCTCCTCCGCCCTCACTATGATTCCTTGTGCGAGCGAAAAC 895

QY 36 -----GlyGlyAsnValIleLysGlyArgThrAspArg---ValPheAsp 49
|||||
896 AGGAGCAACCATACAGCGGGAACACCCGGGAAAGCTAAGGCGGAGAGGCGGATTTGAT 955

QY 50 TrpAsp-----GlySerGlyAspHisArgLeuAsnThrGlnAlaTyrArgIle 65
|||||
956 TGGGATCCTAGCGGTGGTGGTGGTGATCATAGGTTGAATAATCAACCGGAATCGGTT 1015

QY 66 Gly---AsnLeuTyr---SerTrpIleGlyLeuGlnArgHisSerSerGlySerSerTyr 83
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1016 GCGAATAATATGATGCTTCGCTCTAGGGTTGCAAGGCAATCCAGTGGGAGTAGTTTC 1075

QY 84 AspAspSerSerLeuSerSerAspTyrTyrAlaProThrLeuSerAsnProAlaAlaAsn 103
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1076 GGTGAGAGCTCTTTGTCTGGGATTATTACATGCCTACGCTTTCT---GCGGCGGCTAAC 1132

QY 104 GluIleAsnAlaLeuGluTyrIleLeuAspAspPheArgVal----- 118
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QY 119 -----MetLysAlaValGlySerGlyGly---SerSerGlyLys 130
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1193 GGAGGAGATTGAGGATACAGATGCGCGGACTCCGCTGGAGGCTCTCATCTGGGAAG 1252

QY 131 SerTrpAlaGlnGlnThrGluGluSerPheGlnLeuGlnGlnProLeuValLeuArgLeu 150
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1253 AGCTGGCGCAGCAGACGGAGGAGAGTTATCAGCTGCAGCTTGCAATGGCGTTAAGGCTT 1312

QY 151 SerSerAsp**ThrCysAlaAspAspProAsnPheMetAspProIleProAspGluAla 170
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1313 TCGTCGGAGGCTACTTGTGCCGACGATCCGAACCTTCTGGATCCTGTACCGGACGAGTCT 1372

QY 171 AlaLeuArgSerLeuSerIleSerAlaGluAlaIleSerHisArgPheTrp----- 187
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QY 187 ----- 187

DB 1433 CCTGTTAAGCTTTGTTTCCCAAAATATTGAATCGTGGTTATAGAGATATGGTCTCTTG 1492

QY 187 ----- 187

DB 1493 TTTCCGAAGTTTCAGTTAGATCTCCTTACCAAAAGTCTATTAGTAGCAAAATGAGATATGT 1552

QY 188 -----ValAsnGlyCysMe 192
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QY 192 tSerTyrLeuGluLysValProAspGlyPheTyrLeuIleHisGlyMetAspProTyrVa 212
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QY 212 lTrpSerLeuCysThrAsnLeuGlnGluAspGlyArgIleProSerPheGluSerLeuLy 232
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QY 232 sThrValAspSerSerIleGlySerSerIleGluValValIleLeuAspArgHisSerAs 252
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1733 AGCTGTTGATTCGTGTTGATTCTTCGCTTGAAGCGATCATAGTTGATAGGCGTAGTGA 1792

QY 252 pAlaSerLeuLysGluLeuGlnAsnArgValHisAsnIleSerSerCysValThrTh 272

DB 1793 TCCAGCCTTCAAGAACTTCAATAGAGTCCACGACATATCTTGTAGCTGCATTACCAC 1852
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272 rLysGluValAlaAspHisIleAlaLysLeuValCysAsnHisLeuGly----- 288
|||||
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QY 288 ----- 288

DB 1913 ACAATCCTTACTATCCCTTTGAACCTTATATTTTATATCTCTCTGTGATTCTCTCACATTG 1972

QY 289 -----GlySer-ValSerGluGlyGluAspAspLeuValS 300
|||||
1973 TACTCGTTAATCTCTGCTTCCCCAGGGGTCCAGTTATCATGSGGGAAGATGAGTTGGTTC 2032

QY 300 erAlaTrpLysGluCysSerAspAspLeuLysGluCysLeuGlySerAlaValIleProL 320
|||||
2033 CCATGTGGAAGGAGTGCATTTGATGGTCTAAAGAA---ATCTTTAAAGTGGTGGTCCCA 2089

QY 320 euCysSerLeuSerValGlyLeuCysArgHisArgAlaLeuLeuPhe-Lys----- 336
:::
2090 TAGGTAGCCTCTCTGTGGACTCTGCAGACATCGAGCTTTACTCTTCAAAGTGAGATCCC 2149

QY 336 ----- 336

DB 2150 AACTTTGATGCTATCCCATGACATTTAAGACATCTTGTGAAATGATCATATAAATTATT 2209

QY 336 ----- 336

DB 2210 GTGCTTCATCCATTTTGTTTTATTGGAATACATATGAAGAACGTTGAATGTGAAAAGTGG 2269

QY 336 ----- 336

DB 2270 TGTATTGATTAGAAAAAATAGGTTACTGATAGTTGAATGTTCCAAAGAAAAAAGTAT 2329

QY 337 -----ValLeuAlaAspSerIleAspLeuProCysArg 347
|||||
2330 TTTATATCTTCTATTGTTGTCATGCAGGTACTGGCTGACATAATTGATTACCTGTGCGA 2389

QY 348 ileAlaLysGlyCysLysTyrCysThrArgAspAspAlaSerSerCysLeuValArgPhe 367
|||||
2390 ATTGCCAAAGGATGTAATAATATTGTAATAGAGACGATGCCGCTTCGTGCCTTGTGAGTTT 2449

QY 368 GlyLeuAsp----- 370
|||||
2450 GGGCTTGATAGGTATGATACAAGTGATTGCGAAAGAGCCTTTATTTTCTATTTTCTTTG 2509

QY 370 ----- 370

DB 2510 CTTTTTGTCTTGAAAAACAATATATAGCTCCAAATGTTTCGAGAAATATTAGGTTGATG 2569

QY 371 -----ArgGluTyrLeuIleAspLeuIleGlyArgProGly 382
|||||
2570 ACGTGGAAAATTTGTTTGGTTTCAGGGAGTACCTGGTTGATTAGTAGGAAAGCCAGGT 2629

QY 383 CysLeuCysGlnProAspSerLeuLeuAsnGlyProSerSerIleSerIleSerSerPro 402
|||||
2630 CACTTATGGAGCCTGATTCTCTTGTCTAAATGGTCTTTCATCTATCTCAATTTCTTCTCCT 2689

QY 403 LeuArgPheProArgLeuLysProIleGluSerThrIleAspPheArgSerLeuAlaLys 422
|||||
2690 CTGCGGTTTCCACGACCAAGCCAGTTGAACCCGACGTCGATTTTAGGTTACTAGCCAAA 2749

QY 423 GlnTyrPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAlaSer----- 439
|||||
2750 CAATATTTCTCCGATAGCCAGTCTCTTAATCTTGTTTTCGATCCTGCATCAGGTATCCC 2809

QY 439 ----- 439

DB 2810 ATACAAAAAACCTAAATAATATGTTAACTTTTTCATGCTGCTTACATCTCGTTTGTAT 2869

QY 440 -----SerGlyAsnValValSerGlyLysAspAlaAlaPheSerValTyrGlnArg 456
|||||
|||:::|||||

Db 2870 TTCCCTAAAGAGTAATCTCTATCA-----TTTAGGGTATTT----- 2908
QY 457 ProLeuAsnArgLysAspValaspGlyLysThrIleVal----- 469
Db 2909 ---CTTGATCATGTCCTCAGTATCTGAAGTGTAGTAGTCTTAGAATGATCTATTTGTTG 2965
QY 470 -----ValThrGlyAsp----- 473
Db 2966 TTTTCTGTCTCTTTTCACTTTAGTTGTTTTGGCTGTTGATGTGTATGTTTGTGTTGG 3025
QY 474 -----LysAspArgAsnSerGlnLeuLeuAsnLysLysAlaAla 486
Db 3026 GTTCTTGCCTAATGATAATTAAGGTTAAACTTGTAGTCTGCTGTTCAAG----- 3076
QY 487 GlnLeuAsnThrGlnAspGlyLysSerGluGlnPheArgSerCysValAlaSerPro-Ty 506
Db 3077 -----CTTATGAATCTTAGTGCAATTTATGTGCAAGACTTGTCTTCTGGACTCTAAT 3127
QY 506 rSerVal-----GlnSerThrPropheValG1 515
Db 3128 TTCTTATATCTGCTTGTGTTGAATGGTTGTAGATGATATGGATTCTCTCAATGTTTCATAGG 3187
QY 515 uAsn---ValValProLeuSerHisIleSerHisIleGlySerGluAspSerGluHisLe 534
Db 3188 CAATATGATAATCCGGTGGAGAGAAATGACGCATTGG-----CAGAAAATGGT 3235
QY 534 uLeuAlaLeuSerHisProArgMet----- 542
Db 3236 GGTGGGTCCTTGGCCACCCAGTCTAATATGCTCCACAGAACATGATGCGTGGTCAAAAT 3295
QY 543 -----AspHisValAsnAsnLeuPropheValHisGlySerGlnLeuIleArgLy 559
Db 3296 CAAATTGAACGACGACCTATG-AATGCCCCCAACCAATCAGTCAGCCAGTTCACAAACAGGGC 3354
QY 559 sProAsnGluLeuSerLeuGlyLeuGluAspLeuValIleProTrpThrAspLeuAspLe 579
Db 3355 AAATAGGGAACCTGGACTTGATGGTGATGATATGGACATCCCGTGGTGTGATCTTAATAT 3414
QY 579 uArgGluLysIleGlyAla----- 585
Db 3415 AAAAGAAAAGATTGGAGCAGGTAAATATTTTACGGAAAATAATGATTCGGTCTAAAAA 3474
QY 585 ----- 585
Db 3475 TGCAAAGAAATATGAAATCTTTGAGGAAGTGGTTTTGCTTGGACTCTGTTCTCGAACAA 3534
QY 585 ----- 585
Db 3535 AATAAGGAAAAAGTCCACCCATTTTGAGATTACATTCCTCTGTTGCTTTAATCTTT 3594
QY 586 -----GlySerPheGlyThrValTyrArgGlyGluT 596
Db 3595 CCACTCTAATTTGAGCGACTGCTCTTTTCAGGTTCTTTGGCACTGTCCACCGTGTGAGT 3654
QY 596 rpHisGlySer----- 599
Db 3655 GGCATGGCTCGGTAAGAACTTTTTTGTCAGAAATTTACGCAGCTGAATTTTTTTCGCTCT 3714
QY 599 ----- 599
Db 3715 AAAAATTTGGTTGTGACTTTTGGATCTGCTGGTATTATATAAAGGCAAAAGTTATTGTATA 3774
QY 599 ----- 599
Db 3775 TGTGACTCTCCGTTCTGTTCAGAAATTAACACGGACAAAGGTGTCCCATTTTAGATGTA 3834
QY 599 ----- 599
Db 3835 TATGTGCTTTTATATCATAAATTTGTCTCTCTGTTTGAATTTTACAATTTCTATCACTAGA 3894
QY 600 -----AspValAlaValL 604
Db 3895 AGAATCTAAATTTTGATTATTGTCAGTAATAATCTCTATCAATTTTTCAGGATGTTGCTGTGA 3954

QY 604 ysIleLeuThrGluGlnAspPheHisProGluArgValAsnGluPheLeuArgGlu---- 622
Db 3955 AAATTTCTCATGGAGCAAGACTTCCATGCTGAGCGTGTAAATGAGTTCTTAAGAAA-GGTG 4013
QY 622 ----- 622
Db 4014 CACAAATAAAATTTTCTCTTGATTTTGGTAATGAACCTGTTGTATTAAATGCTCCAATGA 4073
QY 623 -----ValAlaIleMetLysSerLeuArgHisProAsnIleValLeuP 637
Db 4074 TCTTGATTGCGTGTGTCAGGTTGCGATAATGAACGCTTCGCCACCCCTAACATTTCTCT 4133
QY 637 heMetGlyAlaValThrLysProProAsnLeuSerIleValThrGluTyrLeuSer---- 655
Db 4134 TCATGGGTGGGTCACTCAACCTCCAAATTTGTCAATAGTGACAGAAATATTGTGTC-AAGG 4192
QY 655 ----- 655
Db 4193 TACAATTACTTGGATTTTGGAAGGTTTGATGTACTGAGTGTAGAATTTTGGCCTATAATGA 4252
QY 656 -----ArgGlySerLeuTyrArgLeuLeuHisLysSerG 667
Db 4253 CTCTAATACCATGATTTCTTTCAACACAGAGGTAGTTATACAGACTTTTTCATAAAAAGTG 4312
QY 667 lyValLysAsp---IleAspGluThrArgArgIleAsnMetAlaPheAspVal----- 683
Db 4313 GAGCAAGGGAGCAATTAGATGAGAGACGTGCGCTGAGTATGGCTTATGATGTGGTATGTT 4372
QY 683 ----- 683
Db 4373 TAACTCCTTATGTATCATGTATGGGTGATTACTTCTCTGATCTTGGTGTTCCTCACATGG 4432
QY 684 -----AlaLysGlyMetAsnTyrLeuHisArgArgAsp 694
Db 4433 AACTTTCTTTCCAAATCTCTGTCAAGGCTAAGGGAATGAATATCTTTCACAATCCCAAT 4492
QY 695 ProProIleValHisArgAspLeuLysSerProAsnLeuLeuValAspLysLysTyrThr 714
Db 4493 CCTCCAATTTGTCATAGAGATCTAAATCTCCAACTTATTGGTTGACAAAAAATATACA 4552
QY 715 ValLysVal----- 717
Db 4553 GTCAAGGT-TTGAATCTAAATTAGAAATTTGTTGTGTCCAATGTTTTTGATTTGATATTTT 4611
QY 717 ----- 717
Db 4612 ATTCCTCTTTGTGAGACAAAGCTTATATATAAAATATGATTTTAAATCTAAATTTGGTTGG 4671
QY 717 ----- 717
Db 4672 AGACATTACAAAAAGGCGTTAATCTGTGTGAAACTTAAAAAGATACAGCAGCCTCAAGCTGT 4731
QY 717 ----- 717
Db 4732 CGTCTTAAAAACAATCAGAACATTTATTATTCTAACTCCTCAATTTGTCTTGAAATTTTCAG 4791
QY 718 ---CysAspPheGlyLeuSerArgLeuLysAlaArgThrPheLeuSerSerLysSerAla 736
Db 4792 GTTTGTGATTTTGGTCTCTCGCGATTGAAGGCCAGCACGTTTTCTTCCTCGAAGTCAGCA 4851
QY 737 AlaGlyThr----- 739
Db 4852 GCTGGAACCGTAAGTTCAGTTTGTGTTTGAACATAAAACACGCTGAACAAACGTAACCTTTCTT 4911
QY 740 -----ProGluTr 742
Db 4912 CTAGGTCTTATTTCCCAATGGAAGCTAAATAAATAACTGACTTTTGATATATCAGCCCGAGTG 4971
QY 742 pMetAlaProGluValLeuArgAspGluProSerAsnGluLysSerAspValTyrSerPh 762
Db 4972 GATGCAACCAAGAGTCTCTCGGAGATGAGCCGCTCTAATGAAAAGTCAGATGTGTACAGCTT 5031

Db 1613 ATCGTACTATGATAAAGTTTCCTGATGGGTTTTTATATCATGAATGGTCTGGATCCCTATAT 1672

Qy 212 lTrpSerLeuCysThrAsnLeuGlnGluAspGlyArgIleProSerPheGluSerLeuLy 232

Db 1673 TTGGACCTTATGCATCGACCTTCGATGAAAGTGTCGATCCCTTCAATTGAATCATTAAG 1732

Qy 232 sThrValAspSerSerIleGlySerSerIleGluValValLeuIleAspArgHisSerAs 252

Db 1733 AGCTGTGATCTCTGGTGTGATCTTCCTCGTTGAAGCGATCATAGTTGATAGCGGTAGTGA 1792

Qy 252 pAlaSerLeuLyGluLeuGlnAsnArgValHisAsnIleSerSerSerCysValThrTh 272

Db 1793 TCCAGCCTTCAAGGAACCTTCACAATAGAGTCCACGACATATCTTGTAGCTGCATTACCAC 1852

Qy 272 rLysGluValAlaAspHisIleAlaLysLeuValCysAsnHisLeuGly 288

Db 1853 AAAAGAGGTGTGATCAGCTGGCAAGCTTATCTGCAATCGTATGGGGTTGTACTCAT 1912

Qy 288 288 288

Db 1913 ACAATCCTTACTATCCCTTTGAACCTTATATTTTATATCTTCTGTGATTTCTCACATTG 1972

Qy 289 289 289

Db 1973 TACTCGTTAAATCTTGCTTCCCGAGGGTCCAGTTATCATGGGGAAAGATGAGTTGGTTC 2032

Qy 300 erAlaTrpLysGluCysSerAspAspLeuLysGluCysLeuGlySerAlaValIleProL 320

Db 2033 CCATGTGGAAGGAGTGCATGTGCTCTAAAAGAA---ATCTTTAAAGTGGTGTTCCTCA 2089

Qy 320 euCysSerLeuSerValGlyLeuCysArgHisArgAlaLeuLeuPhe-Lys- 336

Db 2090 TAGGTAGCCTCTCTGTTGGACTCTGCAGACATCGAGCTTACTCTTCAAAGTGAGATCCC 2149

Qy 336 336 336

Db 2150 AACTTTGATGCTATCCCATGACATTTAAGACATCTTGTGAAATGATCATATAAATTATT 2209

Qy 336 336 336

Db 2210 GTGCTTCATCCATTGTTTTTTATTGGAATACATATGAAGAACGTTGAATGTGAAAAGTGG 2269

Qy 336 336 336

Db 2270 TGTATTGATTAGAAAAAATAGGTTACTGATAGTTGATGTTCCAAAGAAAAAAGTAT 2329

Qy 337 337 337

Db 2330 TTTATATCTTCTATTGTTGGTGCATGCGAGGTACTGGCTGACATAATTGATTTACCTGTCTGA 2389

Qy 348 ileAlaLysGlyCysLysTyrcysThrArgAspAspAlaSerSerCysLeuValArgPhe 367

Db 2390 ATTGCCAAAGGATGTAATATTGTAATAGAGACGATGCCGCTTCGTGCCCTTGTACAGGTTT 2449

Qy 368 GlyLeuAsp- 370

Db 2450 GGGCTTGATAGGTATGATACAAAGTATGCGAAAGAGCCCTTATTTTCCTATTTCCTTTG 2509

Qy 370 370 370

Db 2510 CTTTTTGTTCGGAAAAACAATTATAGCTCCAAATGTTTCGCAGAAATATTAGGTGTATG 2569

Qy 371 371 371

Db 2570 ACGTGGAAAATTGTTTTTGGTTTTCAGGAGTACCTGGTTGATTTAGTAGGAAGCCAGGT 2629

Qy 383 CysLeuCysGlnProAspSerLeuLeuAsnGlyProSerSerIleSerIleSerSerPro 402

Db 2630 CACTTATGGGAGCTGATTCCTTGTCTAAATGGTCCCTTCATCTATCTCAATTTCCTCCT 2689

Qy 403 LeuArgPheProArgLeuLysProIleGluSerThrIleAspPheArgSerLeuAlaLys 422

Db 2690 CTGCGGTTTCCACGACCAAGCCAGTTGAACCCGCGAGTCGATTTAGGTTACTAGCCAAA 2749

Qy 423 GlnTyrPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAlaSer 439

Db 2750 CAATAATTCTCCGATAGCCAGTCTCTTAATCTTGTGTTTCGATCCTGCATCAGGTATTCCC 2809

Qy 439 439 439

Db 2810 ATACAAAAAACCTAAATAATATGTTAACTTTTTTGCAATGCTGTACATCTCGTTTGTAT 2869

Qy 440 440 440

Db 2870 TTCCCTTAAAAAGAGTAATCTCCATCA-----TTTAGGGTATTT----- 2908

Qy 457 ProLeuAsnArgLysAspValAspGlyLysThrIleVal----- 469

Db 2909 ---CTTGATCATGTCAGTATCTCAGTATCTGAAAGTGTTAGTAGTCTAGAAATGATTCTATGTTG 2965

Qy 470 470 470

Db 2966 TTTTCTTGTCTCTTTTCACITTTAGTTGTTTTTGGCTGTTGATGTATGTTTGTGGTGG 3025

Qy 474 474 474

Db 3026 GTTCTTTGCCCTAATGATATTTAAGGTTAAACTTGTTAGTCTGCTGTTCAAG----- 3076

Qy 487 GlnLeuAsnThrGlnAspGlyLysSerGluGlnPheArgSerCysValAlaSerPro-Ty 506

Db 3077 -----CTTATGAATTCTAGTGCATTTATGTGCAAGACTTGTCTTCTGGACTCTAAT 3127

Qy 506 rSerVal-----GlnSerThrProPheValG1 515

Db 3128 TTCTTATATCTGCTTGTGTTGAATGGTTGTAGATGATATGGGATTTCTCAATGTTTCATAGG 3187

Qy 515 uAsn---ValValProLeuSerHisIleSerHisIleGlySerGluAspSerGluHisLe 534

Db 3188 CAATATGATAATCCGGGTGGAGAGAATGACGCATTGG-----CAGAAAATGGT 3235

Qy 534 uLeuAlaLeuSerHisProArgMet----- 542

Db 3236 GGTGGGTCTTTTGCCACCCAGTGCTAATATGCTCCACAGAACATGATGCGTGCCTCAAT 3295

Qy 543 -----AspHisValAsnAsnLeuProPheValHisGlySerGlnLeuIleArgLy 559

Db 3296 CAAATTGAAGCAGCACCTATG-AATGCCCCACCAATCAGTCAGCCAGTTCCAAACAGGGC 3354

Qy 559 sProAsnGluLeuSerLeuGlyLeuGluAspLeuValIleProTrpThrAspLeuAspLe 579

Db 3355 AAATAGGGAACCTGGACTTGATGCTGATGATATGGACATCCCGTGGTGTGATCTTAATAT 3414

Qy 579 uArgGluLysIleGlyAla----- 585

Db 3415 AAAAGAAAAGATTGGAGCAGGTAATAATTTTACGGAAAAAATAATGATTCGGTCTAAAAA 3474

Qy 585 585 585

Db 3475 TGCAAAAGAAATATGAAATTTCTTGAGGAAGTGGTTTTGCTTTGGACTCTGTTCTCGAACAA 3534

Qy 585 585 585

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Qy 596 rpHisGlySer----- 599

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Qy 599 599 599

Db 3715 AAAAATTTGGTTGAGCTTTTGGATCTGCTGGTATTATATAAAGGCAGGTTATTGTGATA 3774

QY 599 ----- 599
Db 3775 TGTGACTCTCCGTTCTGTTCAGAAATTAAACACGGACAAAAGGTGCCAATTTTAGATGTA 3834
QY 599 ----- 599
Db 3835 TATGTGTCTTTATATACATAAAATTGTCCTCTCTGTTTGAATTTTACAATTTCTATCACTAGA 3894
QY 600 ----- 604
Db 3895 AGAATTCTAATTTTGATTATTGCAGTAATANTCTCTATCAATTTTCAAGATGTTGCTGTGA 3954
QY 604 ----- 622
Db 604 YsileLeuThrGluGlnAspPheHisProGluArgValAsnGluPheLeuArgGlu----- 622
Db 3955 AAATTCTCATGGAGCAAGAACTTCCATGCTGAGCGTGTGTAATGAGTCTTTAAGAAA-GGTG 4013
QY 622 ----- 622
Db 4014 CACAAATAAAATTTCTCTTTGATTGTTGGTAATGAACCTTGTGTATTAATGTCTCCAATGA 4073
QY 623 ----- 637
Db 4074 TCTTGATTGCGTGTCTGAGTTGCGATAATGAACGCCCTTCGCCACCCCTAACATTTGTTCTCT 4133
QY 637 heMetGlyAlaValThrLysProProAsnLeuSerIleValThrGluTyrLeuSer---- 655
Db 4134 TCATGGGTGGGTCTCACTCAACCTCCAAATTTGTCAATAGTGACAGAATATTTGTC-AAGG 4192
QY 655 ----- 655
Db 4193 TACAATTACTTGGATTGGAAAGTTTGTATGTAAGTGTAGTGAATTTTGGCCTATAATGA 4252
QY 656 ----- 667
Db 4253 CTCTAATACCATGATTCTTTTCAACACAGAGGTAGTTTATACAGACTTTTGCATAAAAGTG 4312
QY 667 lyValLysAsp---IleAspGluThrArgArgIleAsnMetAlaPheAspVal----- 683
Db 4313 GAGCAAGGGAGCAATTAGATGAGAGACGTCGCTGAGTATGGCTTATGATGTGGTATGTT 4372
QY 683 ----- 683
Db 4373 TAACTCCTTATGTTACATGTATGGTGATTACTTCTGATCTTGGTGTCTTCTCACATGG 4432
QY 684 ----- 694
Db 4433 AACTTTCTTTCCAAATTTCTGTCTCACAGGCTAAGGAATGAATTTATCTTCACAAATCGCAAT 4492
QY 695 ProProIleValHisArgAspLeuLysSerProAsnLeuLeuValAspLysLysTyrThr 714
Db 4493 CCTCCAATTGTGCATAGAGATCTAAATCTCCAAACTTATTTGGTTGACAAAAATATACA 4552
QY 715 VallysVal----- 717
Db 4553 GTCAAGGT-TTGAATCTAAATTAGAAATTTGTTGTCTCCAATGTTTGTATTTTATATTTT 4611
QY 717 ----- 717
Db 4612 ATTCTCTTGTGAGACAAGCTTATATATAAATTATGATTTTAAATTTCTAAATTTGTTGG 4671
QY 717 ----- 717
Db 4672 AGACATTACAAAAAGGCGTTAATCTGTGCTGAACTTAAAGATACAGCAGCCTCAAGCTGT 4731
QY 717 ----- 717
Db 4732 CGTCTTAAAAACAATCAGAACATATTATTCTAACTCCTCAATTTGCTTGAATTTTCAG 4791
QY 718 ---CysAspPheGlyLeuSerArgLeuLysAlaArgThrPheLeuSerSerLysSerAla 736
Db 4792 GTTTGTGATTTTGGTCTCTCGCGAATTGAAGGCCAGCACGTTTCTTCTCGAAGTCAGCA-4851
QY 737 AlaGlyThr----- 739

Db 4852 GCTGGAACCGTAAGTTTCAGTTTGTGTTGAAAACTAAAAACACGCTGAACAACGTAACTTTCTT 4911
QY 740 -----ProGluTr 742
Db 4912 CTAGGTCTTATTTCCAATGGAAGCTAAATAATTACTGACTTTTGATATATCAGCCCGAGTG 4971
QY 742 pMetAlaProGluValLeuArgAspGluProSerAsnGluLysSerAspValTyrSerPh 762
Db 4972 GATGGCACCAGAAAGTCTCGAGATGAGCGGTCTAATGAAAAAGTCAGATGTGTACAGCTT 5031
QY 762 eGlyValIleLeuTyrGluLeuAlaThrLeuGlnGlnProTyrCysAsnLeuAsnProAl 782
Db 5032 CGGGGTCACTTTGTGGAGCTTGTCTACATTCGAACAACCATGGGGTAACTTAAATCCGGC 5091
QY 782 aGln----- 783
Db 5092 TCAGGTACTTCCCACTCTAAACATCCCAATAATAATGATAATTATTGTCATTTTGGAAGT 5151
QY 784 -----Va 784
Db 5152 CCCTCACTCTACATTTTCATAACATGCTATATATGATCATCCACAAAAATGTTCCATAGGT 5211
QY 784 lValAlaAlaValGlyPheLysGlyLysArgLeuAspIleProArgAspValAsnProLy 804
Db 5212 TGTAGCTGGGTGTTTCAAGTGTAACGGCTGGAGATCCCGGCTAATCTGAATCCTCA 5271
QY 804 sLeuAlaSerLeuIleValAlaCysTipAla----- 814
Db 5272 GGTTCAGCCATAATCGAGGTTGTTGGAC-CAAGTACGTTAAGATTTTCTATCTCTTTT 5330
QY 815 -----AspGluProTr 818
Db 5331 TTGAATTTCTTCTTGAATAGACTTCATGTTTATGTATGTGTTTTCATTACCAGTGCATG 5390
QY 818 pLysArgProSerPheSerSerIleMetGluThrLeuLysProMetThrLysGlnAlaPr 838
Db 5391 GAAGGTCCATCATTTGCAACTATAATGGACTTGCTAAGACCATTGATCAATCAGCGGT 5450
QY 838 oProGlnGlnSerArgThrAsp 845
Db 5451 TCCTCCGCCCAACCGCTCGGAT 5472
RESULT 11
US-07-928-464-6
; Sequence 6, Application US/07928464
; Patent No. 5367065
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene and
; TITLE OF INVENTION: Mutations
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
; ADDRESSEE: No. 5367065r1s
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/928,464
; FILING DATE: 19920810
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Suzanne E.
; REGISTRATION NUMBER: 32,279

REFERENCE/DOCKET NUMBER: UPN-1086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 5890 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-928-464-6

Alignment Scores:
Pred. No.: 3.15e-202 Length: 5890
Score: 2068.00 Matches: 555
Percent Similarity: 41.83% Conservative: 111
Best Local Similarity: 34.86% Mismatches: 159
Query Match: 772
DB: 34
Gaps: 1

US-09-904-389-2 (1-850) x US-07-928-464-6 (1-5890)

QY 1 MetGluMetProGlyArgArgSerAspTyrSerLeuLeuSerGlnIleProAspGluGlu 20
DB 354 ATGGAATGCCGGTAGAGATCTAATACACTTTGCTAGTCAATTTCTGACGATCAG 413
QY 21 ValGly-----ThrGlyAlaSerThrSerPheTyrAspSerValAlaAla----- 35
DB 414 GTGTCAAGTTTCGGTCACCGGAGCTCCTCCGCTCACTATGATTCCTTGTCGAGCGAAAC 473
QY 36 -----GlyGlyAsnValIleLysGlyArgThrAspArg---ValPheAsp 49
DB 474 AGGAGCAACCAATAACAGCGGGAACACCGGGAAGCTAAGCGGAGAGAGCGGATTTGAT 533
QY 50 TrpAsp-----GlySerGlyAspHisArgLeuAsnThrGlnAlaTyrArgIle 65
DB 534 TGGGATCCTAGCGGTGGTGGTGGTGATCATAGGTTGAATAATCAACCGGAATCGGGTT 593
QY 66 Gly---AsnLeuTyr---SerTrpIleGlyLeuGlnArgHisSerSerGlySerSerTyr 83
DB 594 GGAATAATATGATGCTTCGTCTCTAGGGTTGCAAGGCAATCCAGTGGGAGTAGTTTC 653
QY 84 AspAspSerSerLeuSerSerAspTyrTyrAlaProThrLeuSerAsnProAlaAlaAsn 103
DB 654 GGTGAGAGCTCTTTGTCTGGGATTTATACATGCCTACGCTTCT---GCGGCGGCTAAC 710
QY 104 GluIleAsnAlaLeuGluTyrIleLeuAspAspAspPheArgVal----- 118
DB 711 GAGATCGAATCTGTGGATTTCTCCTCAAGATGATGGGTTTAGGCTTGATTTGGTGGTGGT 770
QY 119 -----MetLysAlaValGlySerGlyGly---SerSerGlyLys 130
DB 771 GGAGGAGATTTGAGGATACAGATGGCGGCGGACTCCGCTGGAGGGTCTTTCATCTCGGAAG 830
QY 131 SerTrpAlaGlnGlnThrGluGluSerPheGlnLeuGlnGlnProLeuValLeuArgLeu 150
DB 831 AGCTGGGCGCAGCAGCAGGAGAGATTATCAGCTGCAGCTTGCAATTGGCGTTAAGGCTT 890
QY 151 SerSerAsp**ThrCysAlaAspAspProAsnPheMetAspProIleProAspGluAla 170
DB 891 TCGTCGGAGGCTACTTGTGCCGACGATCCGAACCTTTCTGGATCCTGTACCGGACGAGTCT 950
QY 171 AlaLeuArgSerLeuSerIleSerAlaGluAlaIleSerHisArgPheTrp----- 187
DB 951 GCTTTACGGACTTCGCCAAGTTTCAGCCGGAACCGGTTTCACATCGTTTCTGGGTATTGTT 1010
QY 187 ----- 187
DB 1011 CCTGTTAAGCTTTGTTTCCCAAAATTATTGAATCGTGGTTATAGAGATATGGTCTCTTG 1070
QY 187 ----- 187
DB 1071 TTTCCGAAGTTTCAGTTAGATCTCCTTACCAAAAGTCTATTAGTAGCAAAATGAGATATGT 1130

QY 188 -----ValAsnGlyCysMe 192
DB 1131 TGTTTAGATACATTGCAGAGATATGATTTTGTGTGCTGCATCAGGTTAATGGCTGCTT 1190
QY 192 tSerTyrLeuGluLysValProAspGlyPheTyrLeuIleHisGlyMetAspProTyrVa 212
DB 1191 ATCGTACTATGATAAAGTTCCTGATGGGTTTATATGATGAATGGTCTGGATCCCTATAT 1250
QY 212 lTrpSerLeuCysThrAsnLeuGlnGluAspGlyArgIleProSerPheGluSerLeuLy 232
DB 1251 TTGGACCTTATGCATCGACCTGCATGAAAGTGGTCGCAATCCCTTCAATTGAATCATTAAG 1310
QY 232 sThrValAspSerSerIleGlySerSerIleGluValValLeuIleAspArgHisSerAs 252
DB 1311 AGCTGTTGATTTCTGGTGTGATTCTTCGCTTGAAGCGATCATAGTTGATAGGCGTAGTGA 1370
QY 252 pAlaSerLeuLysGluLeuGlnAsnArgValHisAsnIleSerSerSerCysValThrTh 272
DB 1371 TCCAGCCTTCAAGGAACCTTCACATAGAGTCCACGACATATCTTGTAGCTGCATTACCAC 1430
QY 272 rLysGluValAlaAspHisIleAlaLysLeuValCysAsnHisLeuGly----- 288
DB 1431 AAAAGAGGTTGTTGATCAGCTGGCAAAGCTTATCTGCAATCGTATGGGTTTGTACTCAT 1490
QY 288 ----- 288
DB 1491 ACAATCCTTACTATCCCTTTTGAACCTTATATTTTATATCTCTCTGTGATTCTCACATTG 1550
QY 289 -----GlySer-ValSerGluGlyGluAspAspLeuValS 300
DB 1551 TACTCGTTAATTCTTGTCTTCCCGAGGGTCCAGTTATCATGCGGGAAGATGAGTTGGTTC 1610
QY 300 erAlaTrpLysGluCysSerAspAspLeuLysGluCysLeuGlySerAlaValIleProL 320
DB 1611 CCATGTGAAGGAGTGCATTGATGGTCTAAAAGAA---ATCTTTAAAGTGGTGGTTCCTCA 1667
QY 320 euCysSerLeuSerValGlyLeuCysArgHisArgAlaLeuLeuPhe-Lys----- 336
DB 1668 TAGGTAGCCTCTCTGTGGACTCTGCAGACATCGAGCTTTACTCTTCAAAGTGAGATCCC 1727
QY 336 ----- 336
DB 1728 AACTTTGATGCTATCCCATGACATTAAAGACATCTTGTGAAATGATCATATAAATTATT 1787
QY 336 ----- 336
DB 1788 GTGCTTCATCCATTTGTTTTTATTGGAAATACATATGAAGAACGTTGAATGTGAAAAGTGG 1847
QY 336 ----- 336
DB 1848 TGTTATTGATTAGAAAAAATAGTTTACTCATAGTTGAATGTTCCAAAGAAAAAAGTAT 1907
QY 337 -----ValLeuAlaAspSerIleAspLeuProCysArg 347
DB 1908 TTTATATCTTCTATTTGGTGCATGCAGGTACTGGCTGACATAATTGATTACCCCTGTCTGA 1967
QY 348 IleAlaLysGlyCysLysTyrCysThrArgAspAspAlaSerSerCysLeuValArgPhe 367
DB 1968 ATTGCCAAAGGATGTAATAATTGTAATAGACGATGCCGCTTCGCTTGTTCAGGTTT 2027
QY 368 GlyLeuAsp----- 370
DB 2028 GGGCTTGATAGGTATGATACAAGTGATTGCGAAAGAGCCTTTATTTCCTATTTTCTTTG 2087
QY 370 ----- 370
DB 2088 CTTTTTGTCTCGAAAAACAATTATAGCTCCAAATGTTTCGACAAATATTAGTTGTATG 2147
QY 371 -----ArgGluTyrLeuIleAspLeuIleGlyArgProGly 382
DB 2148 ACGTGGAAAAATTTGTTTGGTTTCAGGGAGTACCTGGTTGATTATTAGTAGAAAGCCAGGT 2207

QY 383 CysLeuCysGlnProAspSerLeuLeuAsnGlyProSerSerIleSerIleSerSerPro 402
Db 2208 CACTTATGGAGCGCTGATTCCCTTAAATGGTCCTTCACTATCTCAATTTCTTCCT 2267
QY 403 LeuArgPheProArgLeuLysProIleGluSerThrIleAspPheArgSerLeuAlaLys 422
Db 2268 CTGCGGTTTCCACGACCAAGCCAGTTGAACCCGCGAGTCGATTTAGGTTACTAGCCAAA 2327
QY 423 GlnTyrPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAlaSer 439
Db 2328 CAATATTTCTCCGATAGCCAGTCTCTTAATCTTGTTCGATCCTGCATCAGGTATTCCC 2387
QY 439 439
Db 2388 ATACAAAAAACCTGAATAATATGTTAACTTTTTCATGCTGCTTACATCTCGTTTGTAT 2447
QY 440 -----SerGlyAsnValValSerGlyLysAspAlaAlaPheSerValTyrGlnArg 456
Db 2448 TTCCCTCTAAAAGAGTAATCTCTATCA-----TTAGGGTATTT 2486
QY 457 ProLeuAsnArgLysAspValAspGlyLysThrIleVal 469
Db 2487 ---CTGATCATGCTCAGTATCTGAAGTGTAGTAGTCTTAGAATGATTCTATTGTTTG 2543
QY 470 -----ValThrGlyAsp 473
Db 2544 TTTCTTGTCTCTTTTCACTTTAGTTGTTTGGCTGTTGATGCTATGTTTGTGGTGG 2603
QY 474 -----LysAspArgAsnSerGlnLeuLeuAsnLysLysAlaAla 486
Db 2604 GTTCTTTGCCTAATAGATATTAAGGTTAAACTGTTAGTCTGCTGTTCAAG----- 2654
QY 487 GlnLeuAsnThrGlnAspGlyLysSerGluGlnPheArgSerCysValAlaSerPro-Ty 506
Db 2655 -----CTTATGAATCTAGTGCATTTATGTGCAAGACTTGTCTTGACTCTAAT 2705
QY 506 rSerVal-----GlnSerThrPropheValG1 515
Db 2706 TTCCTATATCTGCTTGTGTAATGTTGTAGATGATATGGGATCTCAATGTTTCATAGG 2765
QY 515 uAsn---ValValProLeuSerHisIleSerHisIleGlySerGluAspSerGluHisLe 534
Db 2766 CAATATGATAATCCGGGTGGAGAGAATGACGCAATGG-----CAGAAATGGT 2813
QY 534 uLeuAlaLeuSerHisProArgMet----- 542
Db 2814 GGTGGGTCCTTGGCACCCAGTCTAATATATGCTCCACAGAACATGATGGGTGCGTCAAAAT 2873
QY 543 -----AspHisValAsnAsnLeuProPheValHisGlySerGlnLeuIleArgLy 559
Db 2874 CAAATTGAGCAGCACCTATG-AATGCCCCACCATCAGTCAGCCAGITCCAAACAGGGC 2932
QY 559 sProAsnGluLeuSerLeuGlyLeuGluAspLeuValIleProTyrPheAspLeuAspLe 579
Db 2933 AAATAGGGAACCTGGACTTGATGGTGATGATATGGACATCCCGTGGTGTGATCTTAATAT 2992
QY 579 uArgGluLysIleGlyAla----- 585
Db 2993 AAAAGAAAAGATTGGAGCAGGTAATAATTTTACGGAAAAAATTAATGATTCGGTCTAAAAA 3052
QY 585 585
Db 3053 TGCAAGAAATATGAAATCTTTGAGGAAGTGGTTTGTGCTTTGGACTCTGTTCTCGAACAA 3112
QY 585 585
Db 3113 AATAAGAAAAAGTGCCACCATTTTGAGATTACATTTCTCTGTTGCTTTAATTTCTT 3172
QY 586 -----GlySerPheGlyThrValTyrArgGlyGluT 596
Db 3173 CCACTCTAATTGAGCGACTGCTCTTTTCAGGTTCTCTTTGGCACTGTCCACCCTGCTGAGT 3232
QY 596 rHisGlySer----- 599

Db 3233 GGCATGGCTCGTAAAGAACTTTTGTGTCAGAAATTTACGCAGCTGAATTTTTCGCTCT 3292
QY 599 599
Db 3293 AAAAAATTGGTTGTGACTTTTGGATCTGCTTGGTATTATATAAAGGCAAGTTATTGTATA 3352
QY 599 599
Db 3353 TGTGACTCTCCGTTCTGTCAAGAAATTAACACGGACAAAGGTGTCCCATTTTAGATGTA 3412
QY 599 599
Db 3413 TATGTGCTTTTATATCATAAATTTGTCTCTCCTGTTTGAATTTTACAAATCTATCACTAGA 3472
QY 600 -----AspValAlaValL 604
Db 3473 AGAATTTCTAATTTTGTATTTGCAGTAATATTCTCTATCAATTTTCAGGATGTTGCTGTA 3532
QY 604 ysIleLeuThrGluGlnAspPheHisProGluArgValAsnGluPheLeuArgGluVal- 623
Db 3533 AAATTTCTCATGGAGCAAGACTTCCATGCTGAGCGTGTAAATGAGTCTTTAAGAGAGGT-G 3591
QY 623 623
Db 3592 CACAAATAAAATTTTCTCTTGTATTTTGGTAATGAACCTTGTGTATTAATGTCTCCAATGA 3651
QY 624 -----AlaIleMetLysSerLeuArgHisProAsnIleValLeuP 637
Db 3652 TCTTGATTCGCTGTGAGTTGCGATAATGAACCGCTTCGCCACCCCTAACATTTGTTCTCT 3711
QY 637 heMetGlyAlaValThrLysProProAsnLeuSerIleValThrGluTyrLeuSer----- 655
Db 3712 TCATGGGTGCGGTCACTCAACCTCCAAATTTGTCAATAGTAGACAGAAATATTTGTC-AAGG 3770
QY 655 655
Db 3771 TACAATTAATTTGGATTTGGAAGGTTTGTATGTAAGTGTAGAAATTTTGGCCTATAATGA 3830
QY 656 -----ArgGlySerLeuTyrArgLeuLeuHisLysSerG 667
Db 3831 CTCTAATACCATGATTTCTTTCAAACAGAGGTAGTTTATACAGACTTTTGCATAAAAGTG 3890
QY 667 lyValLysAsp---IleAspGluThrArgArgIleAsnMetAlaPheAspVal----- 683
Db 3891 GAGCAAGGAGCAATTAGATGAGAGACGTCGCCCTGAGTATGGCTTATGATGTGGTATGTT 3950
QY 683 683
Db 3951 TAACTCCTTATGTTACATGATGGTGATTAATCTCTCTGATCTTGGTGTCTTTCACATGG 4010
QY 684 -----AlaLysGlyMetAsnTyrLeuHisArgArgAsp 694
Db 4011 AACTTTCTTTCCAATTTCTCTGTGCACAGGCTAAGGGAATGAATATCTTCACAATCGCAAT 4070
QY 695 ProProIleValHisArgAspLeuLysSerProAsnLeuValAspLysLysTyrThr 714
Db 4071 CCTCCAATTTGTGCATAGAGATCTAAAAATCTCCAAACTTATTGGTTGACAAAAAATATACA 4130
QY 715 VallysVal----- 717
Db 4131 GTCAAGGT-TTGAATCTAAATTAGAAATTTGTTGTCCAATGTTTGTATTTTGATATTTT 4189
QY 717 717
Db 4190 ATTCTCTTTGTGAGACAAGCTTATATATAAATTAATGATTTTAAATTTCTAAATTTGGTGG 4249
QY 717 717
Db 4250 AGACATTACAAAAAGGCGTTAATCTGCTGAAACTTAAAGACATACAGCAGCCTCAAGCTGT 4309
QY 717 717

Db 4310 CGTCTTAAACAATCAGAACATTATTATTCTAACTCCTCAATTTGTCTTGAAATTCAG 4369
QY 718 ---CysAspPheGlyLeuSerArgLeuLysAlaArgThrPheLeuSerSerLysSerAla 736
Db 4370 GTTTGTGAATTTGGTCTCTCGCGATTGAAGGCCAGCACGTTTCTTCTCCTCGAAGTCAGCA 4429
QY 737 AlaGlyThr----- 739
Db 4430 GCTGGAACCGTAAGTTTCAGTTTGTGAAACTAAACACGCTGAACAACGTAACCTTTCTT 4489
QY 740 -----ProGluTr 742
Db 4490 CTAGGTCCTATTCCAAATGGAAGCTAAATAATTACTGACTTTGATATATCAGCCCGAGTG 4549
QY 742 pMetAlaProGluValLeuArgAspGluProSerAsnGluLysSerAspValTyrSerPh 762
Db 4550 GATGGCACCCAGAGTCCTCGGAGATGAGCCGCTCTAATGAAAGTCAGATGTGTACAGCTT 4609
QY 762 eGlyValIleLeuTrpGluLeuAlaThrLeuGlnGlnProTrpCysAsnLeuAsnProAl 782
Db 4610 CGGGGTCACTTTGTGGAGCTTGCTACATGTCAACCAACCATGGGGTAACCTTAATCCGGC 4669
QY 782 aGln----- 783
Db 4670 TCAGGTACTTCCCACTCTAAACATCCCAATAATAATGATATATTTTGCATTTCGAAAGT 4729
QY 784 -----Va 784
Db 4730 CCCTCACTCTACATTTTCATAACATGCTATATATATGATCATCCAAACAAATGTTCCATAGGT 4789
QY 784 lValAlaAlaValGlyPheLysGlyLysArgLeuAspIleProArgAspValAsnProLy 804
Db 4790 TGTAGCTGCGTTGGTTTCAAGTGTAAACGGCTGGAGATCCCGGTAATCTGAATCCTCA 4849
QY 804 sLeuAlaSerLeuIleValAlaCysTrpAla----- 814
Db 4850 GGTTGCAGCCATAATCGAGGTTGTTGGAC-CAAGTACGTTAAGATTTTCTATCTCTTTT 4908
QY 815 -----AspGluProTr 818
Db 4909 TTGAATCTTCTTGAATAGACTTCATGTTTATGTATGTGTTTCAATFACCAGTGAGCCATG 4968
QY 818 pLysArgProSerPheSerSerIleMetGluThrLeuLysProMetThrLysGlnAlaPr 838
Db 4969 GAAGGTCCTCATCTTTCGAACATAATGGACTTGCTAGACCATGATGATCAATCAGCGGT 5028
QY 838 oProGlnGlnSerArgThrAsp 845
Db 5029 TCCTCCGCCCAACCGCTCGGAT 5050

RESULT 12

PCT-US93-07347-6
; Sequence 6, Application PC/TUS9307347
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene and
; TITLE OF INVENTION: Mutations
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
; ADDRESSEE: Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/07347
FILING DATE: 19930805
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Suzanne E.
REGISTRATION NUMBER: 32,279
REFERENCE/DOCKET NUMBER: UPN-1086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 5890 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US93-07347-6
Alignment Scores:
Pred. No.: 3.15e-202 Length: 5890
Score: 2068.00 Matches: 555
Percent Similarity: 41.83% Conservative: 111
Best Local Similarity: 34.86% Mismatches: 159
Query Match: 46.63% Indels: 772
DB: 5 Gaps: 34
US-09-904-389-2 (1-850) x PCT-US93-07347-6 (1-5890)
QY 1 MetGluMetProGlyArgArgSerAspTyrSerLeuLeuSerGlnIleProAspGluGlu 20
Db 354 ATGGAATGCCCGGTAGAAGATCTAATTACACTTGTCTTAGTCAATTTCTGACGATCAG 413
QY 21 ValGly-----ThrGlyAlaSerThrSerPheTyrAspSerValAlaAla----- 35
Db 414 GTGTCAAGTTTCCGTACCGGAGCTCCTCCGCTCACTATGATTCTCTTCGAGCGAAAC 473
QY 36 -----GlyGlyAsnValIleLysGlyArgThrAspArg---ValPheAsp 49
Db 474 AGGACCAACATAACAGCGGAACACCGGGAAGCTAAGCGGAGAGAGCGGATTGAT 533
QY 50 TrpAsp-----GlySerGlyAspHisArgLeuAsnThrGlnAlaTyrArgIle 65
Db 534 TGGGATCCTAGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 593
QY 66 Gly-----AsnLeuTyr---SerTrpIleGlyLeuGlnArgHisSerSerGlySerSerTyr 83
Db 594 GGGATAATATATGATGCTTCCTCTAGGGTTGCAAGCAATCCAGTGGGAGTAGTTTC 653
QY 84 AspAspSerSerLeuSerSerAspTyrTyrAlaProThrLeuSerAsnProAlaAlaAsn 103
Db 654 GGTCAGAGCTCTTGTCTGGGATATTATACATGCTACGCTTCT---GCGCGGGCTAAC 710
QY 104 GluIleAsnAlaLeuGluTyrIleLeuAspAspPheArgVal----- 118
Db 711 GAGATCGAATCTGTTGGATTCTCTCAAGATGATGGGTTTAGGCTTGGATTGGTGGTGGT 770
QY 119 -----MetLysAlaValGlySerGlyGly---SerSerGlyLys 130
Db 771 GGAGGAGATTGAGGATACAGATGGCGGAGACTCCGCTGGAGGGTCTTCACTCTGGGAAG 830
QY 131 SerTrpAlaGlnGlnThrGluGluSerPheGlnLeuGlnGlnProLeuValLeuArgLeu 150
Db 831 AGCTGGCGCAGCAGACCGGAGAGAGATTATCAGCTGCAGCTTGCATTGGCGTTAAGGCTT 890
QY 151 SerSerAsp***ThrCysAlaAspAspProAsnPheMetAspProIleProAspGluAla 170
Db 891 TCGTCGGAGGCTACTTGTGCCGAGGATCCGAACCTTCTGGATCCTGTACCGGAGAGTCT 950
QY 171 AlaLeuArgSerLeuSerIleSerAlaGluAlaIleSerHisArgPheTrp----- 187
Db 951 GCTTTACGGACTTCGCCAAGTTTCAGCCGAAACCGTTTCACATCGTTTCTGGGTATTGTT 1010
QY 187 ----- 187

Db 1011 CCTGTTAAGCTTTGTTTCCCAAAATATTGAATCGTGGTTATAGAGATATGGTCTCTTG 1070
QY 187 ----- 187
Db 1071 TTTCGGAAGTTTCAGTTAGATCTCCTTACCAAAAGTCTATTAGTAGCAAAATGAGATATGT 1130
QY 188 -----ValAsnGlyCysMe 192
Db 1131 TGTTTAGATACATTCGACAGTAGATGTTGTTGTCGCTGCATCAGGTTAATGGCTGCTT 1190
QY 192 tSerTyrLeuGluLysValProAspGlyPheTyrLeuIleHisGlyMetAspProTyrVa 212
Db 1191 ATCGTACTATGATAAAGTTCCTGATGGGTTTATATGATGAATGGTCTGGATCCCTATAT 1250
QY 212 lTrpSerLeuCysThrAsnLeuGlnGluAspGlyArgIleProSerPheGluSerLeuLy 232
Db 1251 TTGGACCTTATGATCGACCTGCATGAAAGTGGTCGCATCCCTTCAATTGAATCATTAAG 1310
QY 232 sThrValAspSerSerIleGlySerSerIleGluValValLeuIleAspArgHisSerAs 252
Db 1311 AGCTGTTGATTCGGTGTGATTCTTCGCTTGAAGCGATCATAGTTAGTAGCGTAGTGA 1370
QY 252 pAlaSerLeuLysGluLeuGlnAsnArgValHisAsnIleSerSerCysValThrTh 272
Db 1371 TCCAGCCTTCAAGGAACCTTCACAATAGAGTCCACGACATATCTTTAGCTGCATTACCAC 1430
QY 272 rLysGluValAlaAspHisIleAlaLysLeuValCysAsnHisLeuGly----- 288
Db 1431 AAAAGAGGTTGTTGATCAGCTGGCAAGCTTATCTGCAATCGTATGGGGTTTGTACTCAT 1490
QY 288 ----- 288
Db 1491 ACAATCCTTACTATCCCTTTGAACTTATATTTTATATCTTCTGTGATTTCTCACATTG 1550
QY 289 -----GlySer-ValSerGluGlyGluAspAspLeuVals 300
Db 1551 TACTCGTTAATTCTTGCTTCCCGAGGGTCCAGTTATCATGGGGAAGATGAGTTGGTTC 1610
QY 300 erAlaTTrpLysGluCysSerAspAspLeuLysGluCysLeuGlySerAlaValIleProL 320
Db 1611 CCATGTGGAGGAGTGCAATTGATGCTCTAAAAGAA---ATCTTTAAAGTGGTGGTCCCA 1667
QY 320 euCysSerLeuSerValGlyLeuCysArgHisArgAlaLeuLeuPhe-Lys----- 336
Db 1668 TAGGTAGCCTCTCTGTTGGACTCTGCAGACATCGAGCTTACTCTTCAAACTGAGATCCC 1727
QY 336 ----- 336
Db 1728 AACTTTGATGCTATCCCATGACATTTAAGACATCTTGTGAAATGATCATATAAAATTATT 1787
QY 336 ----- 336
Db 1788 GTGCTTCATCCATTGTTTTTTATTGGGAATACATATGAAGAAGCTTGAATGTGAAAAGTGG 1847
QY 336 ----- 336
Db 1848 TGTTATTGATTAGAAAAAATAGGTTACTGATAGTTGAATGTTCCAAAGAAAAAGTAT 1907
QY 337 -----ValLeuAlaAspSerIleAspLeuProCysArg 347
Db 1908 TTTATATCTTCTATTGGTGATGCAGGTACTGGCTGACATAATGATTTACCCCTGTCTGA 1967
QY 348 IleAlaLysGlyCysLysTyrCysThrArgAspAspAlaSerSerCysLeuValArgPhe 367
Db 1968 ATTGCCAAAGGATGTAAATATTGTAATAGACGATGCCGCTTCGTGCTTGTACGCTTT 2027
QY 368 GlyLeuAsp----- 370
Db 2028 GGGCTTGATAGGTATGATACAAGTGATTGCCAAAGAGCCTTTATTTCTTATTTTCTTTG 2087
QY 370 ----- 370

Db 2088 CTTTTTGTCTCTGGAAAAACAATTATATAGCTCCAAATGTTTCGAGATAATTAGGTTGATG 2147
QY 371 -----ArgGluTyrLeuIleAspLeuIleGlyArgProGly 382
Db 2148 AGGTGGAATAATTGTTTGGTTTCAGGGAGTACCTCGTTGATTAGTAGGAAAGCCAGGT 2207
QY 383 CysLeuCysGlnProAspSerLeuLeuAsnGlyProSerSerIleSerIleSerSerPro 402
Db 2208 CACTTATGGGAGCTGATTCCTTGTCTAAATGGTCTCTCATCTATCTCAATTTCTTCTCT 2267
QY 403 leuArgPheProArgLeuLysProIleGluSerThrIleAspPheArgSerLeuAlaLys 422
Db 2268 CTGCGGTTTCCACGACCAAGCCAGTTGAACCCGAGTCGATTTAGGTTACTAGCCAAA 2327
QY 423 GlnTyrPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAlaSer----- 439
Db 2328 CAATATTTCTCCGATAGCCAGTCTCTTAAATCTTGTTTTCGATCCTGCATCAGGTATTCCC 2387
QY 439 ----- 439
Db 2388 ATACAAAAAACCTGAATAATATGTTAACTTTTGCATGCTGCTTACATCTCGTTTGTAT 2447
QY 440 -----SerGlyAsnValValSerGlyLysAspAlaAlaPheSerValTyrGlnArg 456
Db 2448 TTCCCTTAAAGAGTAAATCTCCTATCA-----TTTAGGGTATTT----- 2486
QY 457 ProLeuAsnArgLysAspValAspGlyLysThrIleVal----- 469
Db 2487 ---CTTGATCATGTCCTCAGTATCTGAAGTGTAGTAGTCTTAGAATGATTCTATTGTTG 2543
QY 470 -----ValThrGlyAsp----- 473
Db 2544 TTTTCTGTCTCTTTTTCACCTTAGTTGTTTGGCTGTGTATGTTGTTGGTGG 2603
QY 474 -----LysAspArgAsnSerGlnLeuLeuAsnLysLysAlaAla 486
Db 2604 GTTCTTTGGCTAATGATATTAAAGGTTAAACTTGTAGTCTGCTGTTCAAG----- 2654
QY 487 GlnLeuAsnThrGlnAspGlyLysSerGluGlnPheArgSerCysValAlaSerPro-Ty 506
Db 2655 -----CTTATGAATCTAGTGCATTTATGTGCAAGACTTGTCTTCTGACTCTAAT 2705
QY 506 rSerVal-----GlnSerThrProPheValG1 515
Db 2706 TTCTTATATCTGCTTGTGATGGTTGTAGATGATGGGATTTCTCAATGTTTCATAGG 2765
QY 515 uAsn---ValValProLeuSerHisIleSerHisIleGlySerGluAspSerGluHisLe 534
Db 2766 CAATATGATAATCCGGTGGAGAGATGACGCAATTGG-----CAGAAAAATGGT 2813
QY 534 uLeuAlaLeuSerHisProArgMet----- 542
Db 2814 GGTGGTCTTTGCCACCCAGTGTCTAATATGCTCCACAGAACATGATGCGTGCCTCAAAAT 2873
QY 543 -----AspHisValAsnAsnLeuProPheValHisGlySerGlnLeuIleArgLy 559
Db 2874 CAAATTGAAGCAGCACCTATG-AATGCCCCACCAATCAGTCAGCCAGTTCCAAACAGGGC 2932
QY 559 sProAsnGluLeuSerLeuGlyLeuGluAspLeuValIleProTrpThrAspLeuAsple 579
Db 2933 AAATAGGGAACCTTGGACTTGTATGGTGTATGATATGGACATCCCGTGGTGTGATCTTAATAT 2992
QY 579 uArgGluLysIleGlyAla----- 585
Db 2993 AAAAGAAAAGATTGGAGCAGGTAATAAATTTACGAAAAAATTAATGATTCGGTCTAAAAA 3052
QY 585 ----- 585
Db 3053 TGCAAGAAATATGAAATTTCTTGAGGAAGTGGTTTGTCTTTGGACTCTGTTCTCGAACAA 3112
QY 585 ----- 585
Db 3113 AATAAGGAAAAAGTGCACCCCATTTTGTAGATTACATTTCTTCTGTGCTTAAATCTT 3172

QY	586	-----GlySerPheGlyThrValTyrArgGlyGluT	596
Db	3173	CCACTCTAATTGAGCGACTGCTCTTTCAGGTTCCCTTTGGCACTGTCCACCGTGTCTGAGT	3232
QY	596	rpHisGlySer-----	599
Db	3233	GGCATGGCTCGGTAAGAAGCTTTTTTGTGCAGAAATTTACGCAGCTGAATTTTTTTTCGCTCT	3292
QY	599	-----	599
Db	3293	AAAAATTTGGTTGTGACTTTTGGATCTGCTTGGTATTATAAAGGCAAGATTATTGTGATA	3352
QY	599	-----	599
Db	3353	TGTGACTCTCCGTTCTGTGCAGAAATTAACACACGGACAAAAGGTGTCTCCATTTTAGAATGA	3412
QY	599	-----	599
Db	3413	TATGTGCTTTATATCATAAATTTGTCTCTCTGTTTGAATTTTACAATTTCTATCACTAGA	3472
QY	600	-----AspValAlaValL	604
Db	3473	AGAATTCCTAATTTTGATTATTGTCAGTAATATTCTCTATCAATTTTCAGGATGTTGCTGTGA	3532
QY	604	ysIleLeuThrGluGlnAspPheHisProGluArgValAsnGluPheLeuArgGluVal-	623
Db	3533	AAATTTCTCATGGAGCAAGACTTCCATGCTGAGCGTGTAAATGAGTCTTTAAGAGAGGT-G	3591
QY	623	-----	623
Db	3592	CACAAATAAAATTTTCTCTTGATTTTGGTAATGAACCTTGTGTATTATAATGTCTCCAATGA	3651
QY	624	-----AlaIleMetLysSerLeuArgHisProAsnIleValleuP	637
Db	3652	TCTTGATTCCGCTGCTCAGGTTGCGATAATGAACGCCCTTCGCCACCCCTAACATTTGTTCTCT	3711
QY	637	heMetGlyAlaValThrLysProProAsnLeuSerIleValThrGluTyrLeuSer----	655
Db	3712	TCATGGTGCGGTCACTCAACCTCCAAATTTGTCAATAGTGACAGAAATATTGTGTC-AAGG	3770
QY	655	-----	655
Db	3771	TACAATTACTTGGATTGGAAGGTTTGATGTAAGTGTAGAGTGTAGAAATTTTGGCCTATAATGA	3830
QY	656	-----ArgGlySerLeuTyrArgLeuLeuHisLysSerG	667
Db	3831	CTCTAATACCATGATTTCTTTCAAACAGAGAGTAGTTTATACAGACTTTTTCATATAAAAGTG	3890
QY	667	lyValLysAsp---IleAspGluThrArgArgIleAsnMetAlaPheAspVal-----	683
Db	3891	GAGCAAGGAGCAATTACATGAGAGACGTCGCCTGAGTATGGCTTATGATGTGGTATGTT	3950
QY	683	-----	683
Db	3951	TAACTCCTTATGTTACATGTATGGGTGATTACTTCTCTGATCTTGGTGTCTTCTCACATGG	4010
QY	684	-----AlaLysGlyMetAsnTyrLeuHisArgArgAsp	694
Db	4011	AACTTTCTTTCCAATTTCTGTCTCACAGGCTAAGGGAATGAATTATCTTTCACAAATCGCAAT	4070
QY	695	ProProIleValHisArgAspLeuLysSerProAsnLeuLeuValAspLysLysTyrThr	714
Db	4071	CCTCCAATTTGTGCATAGACATCTAAATCTCCAACTTATTGGTTGACAAAAAATATACA	4130
QY	715	VallysVal-----	717
Db	4131	GTCAAGGT-TTGAATCTAAATTAGAAATTTGTTGTGTCCAAATGTTTGTGATTTTGTATATTTT	4189
QY	717	-----	717
Db	4190	ATTCTCTTTGTGAGACAAGCTTATATATAAATTAATGATTTTAAATTTCTAAATTCGTTTGG	4249

QY	717	-----	717
Db	4250	AGACATTACAAAAAGCGTTAATCTGCTGAAACTTAAAGATACAGCAGCCTCAAGCTGT	4309
QY	717	-----	717
Db	4310	CGTCTAAAAACAATCAGAACATTATTCTTAACCTCTCAATTTGTCTTGAAATTTTCAG	4369
QY	718	---CysAsppheGlyLeuSerArgLeuLysAlaArgThrPheLeuSerSerLysSerAla	736
Db	4370	GTTCGTGAATTTGGTCTCTCGCGATTGAAGGCCAGCACGTTCTCTTCTCGAAGTCAGCA	4429
QY	737	AlaGlyThr-----	739
Db	4430	GCTGGAAACCGTAAGTTCAGTTTGTGTTGAAACTAAACACGCTGAACAACGTAACTTTCTT	4489
QY	740	-----	742
Db	4490	CTAGGTCTATTTCCAATGGAAGCTAAATAATTACTGACTTTTGATATATCAGCCCGAGTG	4549
QY	742	pMetAlaProGluValLeuArgAspGluProSerAsnGluLysSerAspValTyrSerPh	762
Db	4550	GATGGCACCAAGAAGTCTCTCGAGATGAGCCGCTCTAATGAAAAAGTCAGATGTGTACAGCTT	4609
QY	762	eGlyValIleLeuTrpGluLeuAlaThrLeuGlnGlnProTrpCysAsnLeuAsnProAl	782
Db	4610	CGGGGTCACTCTTGTGGGAGCTTGTCTACATTGCAACAACCATGGGGTAACTTAATCCGGC	4669
QY	782	agln-----	783
Db	4670	TCAGGTACTCCCACTCTAAACATCCCAAATAATAATGATATTATTTTGCATTTTGGAAGT	4729
QY	784	-----	784
Db	4730	CCCTCACTCTACATTTTCATAACATGCTATATATGATCATCCAAACAAATGTTCCATAGGT	4789
QY	784	lValAlaValGlyPheLysGlyLysArgLeuAspIleProArgAspValAsnProLy	804
Db	4790	TGTAGCTGCGGTGGTGTTCAGGTGTAACCGCTGGAGATCCCGCGTAACTCTGAATCCTCA	4849
QY	804	sLeuAlaSerLeuIleValAlaCysTrpAla-----	814
Db	4850	GGTTGCAGCCATAATCGAGGGTTGTTGGAC-CAAGTACGTTAAGATTTTCTATCTCTTTT	4908
QY	815	-----	815
Db	4909	TTGAATTTCTTCTCAATAGACTTCATGTTTATGTATGTGTTTCATTACCAGTGAGCCATG	4968
QY	818	pLysArgProSerPheSerSerIleMetGluThrLeuLysProMetThrLysGlnAlaPr	838
Db	4969	GAAGCGTCCATTCATTTGCAACTATAATGGAAGTCTGCTAAGACCATTGATCAAAATCAGCGGT	5028
QY	838	oProGlnGlnSerArgThrAsp	845
Db	5029	TCCTCCGCCCAACCGCTCGGAT	5050
RESULT 13			
US-08-003-311B-6			
; Sequence 6, Application US/08003311B			
; Patent No. 5444166			
; GENERAL INFORMATION:			
; APPLICANT: Ecker, Joseph R.			
; APPLICANT: Kieber, Joseph J.			
; TITLE OF INVENTION: Constitutive Triple Response Gene			
; TITLE OF INVENTION: and Mutations			
; NUMBER OF SEQUENCES: 13			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and			
; ADDRESSEE: No. 5444166ris			
; STREET: One Liberty Place - 46th Floor			
; CITY: Philadelphia			
; STATE: PA			
; COUNTRY: U.S.A.			

QY	348	IleAlaIysGlyCysLysTyrCysThrArgAspAspAlaSerSerCysLeuValArgPhe	367	QY	579	uArgGluLysIleGlyAla	585
DB	2390	ATTGCCAAAGGATGTAATATGTAATAGACAGCATGCCGCTTCGTGCTTGTCAAGTTT	2449	DB	3415	AAAAGAAAAGATTGGAGCAGGTAATAATTTTACGGAAAAAATAATGATTCGGTCTAAAAA	3474
QY	368	GlyLeuAsp	370	QY	585		585
DB	2450	GGGCTTGATAGGTATGATACAAAGTGATTGCGAAAGAGCCTTTATTTCTCTATTTCTTTG	2509	DB	3475	TGCAAGAGAAATATGAAATTCCTTGAGGAAGTGTTTTTTCCTTTTGGACTCTGTTCCTCGAACA	3534
QY	370		370	QY	585		585
DB	2510	CTTTTGTCTTCTGAAAACAATATATAGCTCCAAATGTTTCGCAGAATATTAGTTTGATG	2569	DB	3535	AATAAGGAAAAAGTGCCACCCATTTTGAGATTACATTTCTCTCTGTTCCTTTAATTTCTT	3594
QY	371		382	QY	586		596
DB	2570	ACGTGGAAAAATTTGTTTTGTTTCAGGGAGTACTGGTTGATTTAGTAGGAAAGCCAGGT	2629	DB	3595	CCACTCTAATTTGAGCGACTGCTCTTTTCAGGTTCTTTTGGCACTGTCCACCGTGTCTGAGT	3654
QY	383	CysLeuCysGlnProAspSerLeuLeuAsnGlyProSerSerIleSerIleSerSerPro	402	QY	596	rpHisGlySer	599
DB	2630	CACATTATGGGAGCCTGATCTCTTGTCTAAATGGTCCTTCATCTATCTCAATTTCTTCTCT	2689	DB	3655	GGCATGGCTCGGTAAGAACTTTTTTGTGCAGAAATTTACGCAGCTGAATTTTTTTTCGCTCT	3714
QY	403	LeuArgPheProArgLeuLysProIleGluSerThrIleAspPheArgSerLeuAlaLys	422	QY	599		599
DB	2690	CTCGGGTTCCACGACCAAGCCAGTTGAACCCCGAGTCGATTTTAGTTACTAGCCAAA	2749	DB	3715	AAAAATTTGGTTGTGACTTTTGGATCTGCTGGTATTATAAAAGGCAAGTTATTGTATA	3774
QY	423	GlnTyrPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAlaSer	439	QY	599		599
DB	2750	CAATATTCTCCGATAGCCAGTCTCTTAATCTTGTTCGATCCTGCATCAGGTATTCCTC	2809	DB	3775	TGTGACTCTCCGTTCTGTGCAGAAATTAACACGGACAAAAGGTGTCCCATTTTGTAGATGA	3834
QY	439		439	QY	599		599
DB	2810	ATACAAAAAACCTAAATAATATGTTAACTTTTTGCGATGCTGCTTACATCTCGTTTGTAT	2869	DB	3835	TATGTCTCTTTATATCATAAATTTGTCTTCTCTGTTTGAATTTTACAAATTTCTATCCTAGA	3894
QY	440		456	QY	600		604
DB	2870	TTCCCTTAAAGAGTAACTCTCTATCA	2908	DB	3895	AGAAATCTAATTTTGAATTATTGTCAGTAATATCTCTATCAATTTTCAGGATGTTGCTGGA	3954
QY	457	ProLeuAsnArgLysAspValAspGlyLysThrIleVal	469	QY	604	ysIleLeuThrGluGlnAspPheHisProGluArgValAsnGluPheLeuArgGluVal	623
DB	2909	CTTGATCATGTCCTCAGTATCTGAAGTGTAGTAGTCTTAGAATGATCTATTGTTTG	2965	DB	3955	AAATTCATCATGGAGCAAGACTTCCATGCTGAGCGTGTTAATGAGTTCTTAAGAGAGGT-G	4013
QY	470		473	QY	623		623
DB	2966	TTTTCTTGCTCTTTTCACTTTTAGTGTGTTTTGGCTGTGATGTGATGTTGTTGGTGG	3025	DB	4014	CACAAATAAAATTTTCTCTTGATTTTGGTAATGAACCTTGTGTATTAATGTTCTCCAATGA	4073
QY	474		486	QY	624		637
DB	3026	GTCTTTGCTTAATGATATTTAAGTTAACTTGTAGTCTGCTGTTCAAG	3076	DB	4074	TCTTGATTCGCTGTGAGTTGCGATAATGAACCGCTTCGCCACCCCTAACATTTGTTCTCT	4133
QY	487	GlnLeuAsnThrGlnAspGlyLysSerGluGlnPheArgSerCysValAlaSerPro-Ty	506	QY	637	heMetGlyAlaValThrLysProProAsnLeuSerIleValThrGluTyrLeuSer	655
DB	3077	CTTATGAATTTCTAGTGCAATTTATGTGCAAGACTGTCTTCTGCACTCTAAT	3127	DB	4134	TCAATGGGTGCGTCACTCAACCTCCAAATTTGTCAATAGTGACAGAAATATTGTC-AAGG	4192
QY	506	rSerVal	515	QY	655		655
DB	3128	TTCTTATATCTGCTGTTTGAATGGTTGTAGATGATATGGGATTTCTCAATGTTTCATAGG	3187	DB	4193	TACAATTACTTGGATTTTGGAGGTTTGATGTACTAGTGATAGAATTTTGGGCTATAATGA	4252
QY	515	uAsn	534	QY	656		667
DB	3188	CAATATGATAATCCGGTGGAGAGATGACGCAATGG	3235	DB	4253	CTCTAATACCATGATTTCTTTCAAACAGAGGTAGTTTATACAGACTTTTGCATAAAAGTG	4312
QY	534	uLeuAlaLeuSerHisProArgMet	542	QY	667	lyValLysAsp	683
DB	3236	GGTGGGTCTTTTGCACCCAGTGCTAATATGCTCCACAGAACATGATGCGTGGCTCAAAT	3295	DB	4313	GAGCAAGGAGCAATTAGATGACAGACGTCGCTGAGTATGGCTTATGATGTGATGTT	4372
QY	543		559	QY	683		683
DB	3296	CAAAATTGAAGCAGCACCTATG-AATGCCCCACCAATCAGTCAGCCAGTTCCAAACAGGGC	3354	DB	4373	TAACTCCTTATGTTACATGTATGGGTGATTACTTCTCTGATCTTGGTGTGTTTTCACATGG	4432
QY	559	sProAsnGluLeuSerLeuGlyLeuGluAspLeuValIleProTrpThrAspLeuAspLe	579	QY	684		694
DB	3355	AAATAGGGAACCTTGACTTGATGGTATGATATGGACATCCCGTGGTGTGATCTTAATAT	3414	DB	4433	AACTTTCTTCCAAATTTCTCTGTACAGGCTAAGGGAATGAATTTATCTTCAATCGCAAT	4492
QY				QY	695	ProProIleValHisArgAspLeuLysSerProAsnLeuLeuValAspLysLysTyrThr	714

Db 4493 CCTCCAATTGTGCATAGATCTAAATCTCCAAACITATTGGTTGACAAAAATATACA 4552
QY 715 Vallysval----- 717
Db 4553 GTCAAGGT-TGAATCTAAATTAGAAATTGTTGTGCCAATGTTTGTATTTTGATATTT 4611
QY 717 ----- 717
Db 4612 ATTCTCTTGTGAGACAAGCTTATATATAAATTATGATTTTAAATCTCTAAATTTGGTTGG 4671
QY 717 ----- 717
Db 4672 AGACATTACAAAAAGCGTTAATCTGTCTGAAACTTAAAGATACAGCAGCCTCAAGCTGT 4731
QY 717 ----- 717
Db 4732 CGTCTTAAAAACAATCAGAACATTATTATTCTTAACCTCCTCAATTTGTCTTGAAATTCAG 4791
QY 718 ---CysAspPheGlyLeuSerArgLeuLysAlaArgThrPheLeuSerSerLysSerAla 736
Db 4792 GTTTGTGAATTTGGTCTCTCGGATTGAAGCCAGCACGTTTCTTCTCGAAGTCAGCA 4851
QY 737 AlaGlyThr----- 739
Db 4852 GCTGGAACCGTAAGTTCAGTTTGTGTTGAACTAAAAACAGCTGTAACAACGTAACITTTCT 4911
QY 740 -----ProGluTr 742
Db 4912 CTAGGTCCTATTTCCAATGGAAGCTAAATAATTACTGACTTTGATATATCAGCCCCGAGTG 4971
QY 742 pMetAlaProGluValLeuArgAspGluProSerAsnGluLysSerAspValTySerPh 762
Db 4972 GATGCCACCAGAAAGTCTCGCAGATGAGCCGCTCTAATGAAAGTCAGATGTGTACAGCTT 5031
QY 762 eGlyValIleLeuTrpGluLeuAlaThrLeuGlnGlnProTrpCysAsnLeuAsnProAl 782
Db 5032 CGGGTTCATCTTGTGGAGCTTGCTACATTGCAACAACCATGGGGTAACCTTAAATCCGGC 5091
QY 782 aGln----- 783
Db 5092 TCAGGTACTTCCACTCTAAACATCCCAATAATAATGATATTATTGTCATTGGAAGT 5151
QY 784 -----Va 784
Db 5152 CCCTCACTCTACATTTTCATAACATGCTATATATGATCATCCAAACAAATGTTCCATAGGT 5211
QY 784 lValAlaAlaValGlyPheLysGlyLysArgLeuAspIleProArgAspValAsnProLy 804
Db 5212 TGTAGCTGGGTTGGTTTCAAGTGTAAACGGCTGGAGATCCCGGTAATCTGAATCCTCA 5271
QY 804 sLeuAlaSerLeuIleValAlaCysTrpAla----- 814
Db 5272 GGTTCAGCCATAAATCGAGGGTTGTTGGAC-CAAGTACGTTAAGATTTTCTATCTCTTTT 5330
QY 815 -----AspGluProTr 818
Db 5331 TTGAATTCTTCTGAATAGACTTCATGTTTATGATGTTGTTTTCATTACCAGTCAGCCATG 5390
QY 818 pLysArgProSerPheSerIleMetGluThrLeuLysProMetThrLysGlnAlaPr 838
Db 5391 GAAGCGTCCATCATTTGCAACTATATATGACCTTGCTAAGACCATTTGATCAAAATCAGCGGT 5450
QY 838 oProGlnGlnSerArgThrAsp 845
Db 5451 TCCTCCGCCCAACCGCTCGGAT 5472

RESULT 14
US-08-261-432-6
; Sequence 6, Application US/08261432
; Patent No. 5602322
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.

APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene
TITLE OF INVENTION: and Mutations
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: No. 5602322ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,432
FILING DATE: June 17, 1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/003,311
FILING DATE: January 12, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: UPN-1864
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 6312 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-261-432-6

Alignment Scores:
Pred. No.: 3.54e-202 Length: 6312
Score: 2068.00 Matches: 555
Percent Similarity: 41.83% Conservative: 111
Best Local Similarity: 34.86% Mismatches: 159
Query Match: 46.63% Indels: 772
DB: 1 Gaps: 34

US-09-904-389-2 (1-850) x US-08-261-432-6 (1-6312)

QY 1 MetGluMetProGlyArgArgSerAspTyrSerLeuLeuSerGlnIleProAspGluGlu 20
Db 776 ATGGAATGCCCGGTAGAGATCTAATTACACTTTGCTTAGTCAATTTCTGACGATCAG 835
QY 21 ValGly-----ThrGlyAlaSerThrSerPheTyrAspSerValAlaAla----- 35
Db 836 GTGTCAAGTTCCGTCACCGGAGCTCCTCCGCTCACTATGATTCCTTGTTCGAGCGAAAC 895
QY 36 -----GlyGlyAsnValIleLysGlyArgThrAspArg---ValPheAsp 49
Db 896 AGGAGCAACCATAAACAGCGGGAACACCGGAAAGCTAAGCGGAGAGAGCGGATTTGAT 955
QY 50 TrpAsp-----GlySerGlyAspHisArgLeuAsnThrGlnAlaTyrArgIle 65
Db 956 TGGGATCCTAGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1015
QY 66 Gly---AsnLeuTyr---SerTrpIleGlyLeuGlnArgHisSerSerGlySerSerTyr 83
Db 1016 GGAATAATATGATGCTTTCGCTCTAGGGTTGCAAGGCAATCCAGTGGGAGTAGTTTC 1075
QY 84 AspAspSerSerLeuSerSerAspTyrTyrAlaProThrLeuSerAsnProAlaAlaAsn 103
Db 1076 GGTGAGAGCTCTTTGCTCTGGGATTATTACATGCCTACGCTTCT---GCGGCGGCTAAC 1132

QY	104	GlulIeAsnAlaLeuGluTyrIleLeuAspAspPheArgVal	-----	118
Db	1133	GAGATCGAATCTGTTGGATTTCCTCAAGATGATGGGTTTAGGCTTGGATTGGTGGTGGT	1192	
QY	119	-----MetLysAlaValGlySerGlyGly---SerSerGlyLys	130	
Db	1193	GGAGGAGATTGAGGATACAGATGGCGCGGACTCCGCTGGAGGCTTTCATCTGGGAAG	1252	
QY	131	SerTrpAlaGlnGlnThrGluGluSerPheGlnLeuGlnGlnProLeuValLeuArgLeu	150	
Db	1253	AGCTGGCGCAGCAGACGGAGGAGATTATCAGCTGCAGCTTGCAATTGGCGTTAAGGCTT	1312	
QY	151	SerSerAsp***ThrCysAlaAspAspProAsnPheMetAspProIleProAspGluAla	170	
Db	1313	TCGTCGGAGGCTACTTGTGCCGACGATCCGAACCTTTCTGGATCCTGTACCGACGAGTCT	1372	
QY	171	AlaLeuArgSerLeuSerIleSerAlaGluAlaIleSerHisArgPheTrp	187	
Db	1373	GCTTTACGGACTTCGCCAAGTTCAGCCGAAACCGTTTTCACATCGTTCTGGGTATTGTT	1432	
QY	187	-----	187	
Db	1433	CCTGTTAAGCTTTGTTTCCCAAAATTATTGAATCGTGGTTATAGAGATATGGTCCCTCTTG	1492	
QY	187	-----	187	
Db	1493	TTTCCGAAGTTTCAGTTAGATCTCCTTACC AAAAGTCTATTAGTAGCAAAATGAGATATGT	1552	
QY	188	-----ValAsnGlyCysMe	192	
Db	1553	TGTTTAGATACATTGCAGAGTATGATTGTTTGTGTGCTGCATCAGGTTAATGGCTGCTT	1612	
QY	192	tSerTyrLeuGluLysValProAspGlyPheTyrLeuIleHisGlyMetAspProTyrVa	212	
Db	1613	ATCGTACTATGATAAAGTTCCTGTATGGGTTTATATGATGAATGGTCTGGATCCCTATAT	1672	
QY	212	lTrpSerLeuCysThrAsnLeuGlnGluAspGlyArgIleProSerPheGluSerLeuLy	232	
Db	1673	TTGGACCTTATGCAATCGACCTGCATGAAAGTGGTGCATCCCTTCAATTGAATCATTAAG	1732	
QY	232	sThrValAspSerSerIleGlySerSerIleGluValValLeuIleAspArgHisSerAs	252	
Db	1733	AGCTGTTGATTCTGGTGTGATTCTTCGGTTGGAAGCGATCATAGTTGATAGCGGTAGTGA	1792	
QY	252	pAlaSerLeuLysGluLeuGlnAsnArgValHisAsnIleSerSerSerCysValThrTh	272	
Db	1793	TCCAGCCTTCAAGGAACCTTCACAATAGAGTCCACGACATATCTTGTAGCTGCATTACCAC	1852	
QY	272	rLysGluValAlaAspHisIleAlaLysLeuValCysAsnHisLeuGly	288	
Db	1853	AAAAGAGGTTGTTGATCAGTGGCAAAGCTTATCTGCAATCGTATGGGGTTGTACTCAT	1912	
QY	288	-----	288	
Db	1913	ACAATCCTTACTATCCCTTTGAACCTTATATTTTATATCTTCTGTGATTTCTCACATTG	1972	
QY	289	-----GlySer-ValSerGluGlyGluAspAspLeuValS	300	
Db	1973	TACTCGTTAATTCTTGTCTCCCGAGGGTCCAGTTATCATGGGGAAGATGATGGTTC	2032	
QY	300	erAlaTrpLysGluCysSerAspAspLeuLysGluCysLeuGlySerAlaValIleProL	320	
Db	2033	CCATGTGGAAGGAGTGCAATTGATGGTCTAAAGAA---ATCTTTAAAGTGGTGGTTC	2089	
QY	320	euCysSerLeuSerValGlyLeuCysArgHisArgAlaLeuLeuPhe-Lys	336	
Db	2090	TAGGTAGCCTCTCTGTTGGACTCTGCAGACATCGAGCTTTACTCTTCAAAGTGAGATCCC	2149	
QY	336	-----	336	
Db	2150	AACTTTGATGCTATCCCATGACATTTAAGACATCTTGTGAAATGATCATATAAAATTATT	2209	

QY	336	-----	336
Db	2210	GTGCTTCATCCATTGTTGTTTATTGGAATACATATGAAGAACGTTGAATGTGAAAAAGTGG	2269
QY	336	-----	336
Db	2270	TGTTATTGATTAGAAAAAATAGGTTACTGTATAGTTGAATGTTCCAAAAAGAAAAAGTAT	2329
QY	337	-----ValLeuAlaAspSerIleAspLeuProCysArg	347
Db	2330	TTTATATCTTCTATTGGTGCGAGGCTACTGGCTGACATAAATGATTTACCCCTGTGCGA	2389
QY	348	IleAlaLysGlyCysLysTyrCysThrArgAspAspAlaSerSerCysLeuValArgPhe	367
Db	2390	ATTGCCAAAGGATGTAATATGTAATAGAGACGATCCGCTTCGTGCTTGTTCAGGTTT	2449
QY	368	GlyLeuAsp-----	370
Db	2450	GGGCTTGATAGGTATGATACAAAGTGATTGCGAAAGAGCCTTATTATTTCTATTCTTTG	2509
QY	370	-----	370
Db	2510	CTTTTGTGTTCTGGAAAAACAATTATAGCTCCAAATGTTTCGACAGAAATATTAGGTTGATG	2569
QY	371	-----ArgGluTyrLeuIleAspLeuIleGlyArgProGly	382
Db	2570	ACGTGGAATAATTTGTTTGGTTTTCAGGAGTACCTGGTTGATTAGTAGGAAAGCCAGGT	2629
QY	383	CysLeuCysGlnProAspSerLeuLeuAsnGlyProSerSerIleSerIleSerSerPro	402
Db	2630	CACATTATGGGAGCCTGATTCCTTCGCTAAATGGTCCCTTCATCTATCTCAATTTCTTCTCT	2689
QY	403	LeuArgPheProArgLeuLysProIleGluSerThrIleAspPheArgSerLeuAlaLys	422
Db	2690	CTGCGGTTTCCACGACCAAGCCAGTTGAACCCGCGAGTCGATTTAGGTTACTAGCCAAA	2749
QY	423	GlnTyrPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAlaSer-----	439
Db	2750	CAATATTCTCCGATAGCCAGTCTCTTAATCTTGTGTTTCGATCCTGCATCAGGTATTCCC	2809
QY	439	-----	439
Db	2810	ATACAAAAAACCTAAATAATATGTTAACTTTTTCATGCTGCTTACATCTCGTTTGTAT	2869
QY	440	-----SerGlyAsnValValSerGlyLysAspAlaAlaPheSerValTyrGlnArg	456
Db	2870	TTCCCTTAAAGAGTAATCTCCTATCA-----TTTAGGGTATTT-----	2908
QY	457	ProLeuAsnArgLysAspValAspGlyLysThrIleVal-----	469
Db	2909	---CTTGATCATGCTCAGTATCTCAGTATCTGAAGTGTAGTAGTCTTAGAATGATCTATTGTTG	2965
QY	470	-----ValThrGlyAsp-----	473
Db	2966	TTTTCTGTCTCTTTTCACTTTTAGTTGTTTGGCTGTTGATGTGTATGTTGTTGGTGG	3025
QY	474	-----LysAspArgAsnSerGlnLeuLeuAsnLysLysAlaAla	486
Db	3026	GTTCTTTGCCTAATGATATTAAAGGTTAAACTGTTAGTCTGCTGTTCAAG-----	3076
QY	487	GlnLeuAsnThrGlnAspGlyLysSerGluGlnPheArgSerCysValAlaSerPro-Ty	506
Db	3077	-----CTTATGAATCTAGTGCATTTATGTGCAAGACTTGTCTCTTCGGACTCTAAT	3127
QY	506	rSerVal-----GlnSerThrProPheValG1	515
Db	3128	TTCTTATATCTGCTGTTTGAATGGTTGTAGATGATATGGGATTTCTCAATGTTTCATAGG	3187
QY	515	uAsn---ValValProLeuSerHisIleSerHisIleGlySerGluAspSerGluHisLe	534
Db	3188	CAATATGATAATCCGGGTGGAGAGAAATGACGCATTGG-----CAGAAAAATGGT	3235
QY	534	uLeuAlaLeuSerHisProArgMet-----	542

Db 3236 GGTGGGCTCTTTGCCACCCAGTGTAAATATGCCTCCACAGACATGATGCGTGCCTCAAAT 3295
Qy 543 -----AspHisValAsnAsnLeuPropheValHisGlySerGlnLeuLeuLeuArgLy 559
Db 3296 CAAATTGAAGCAGCAGCCTATG-AATGCCCCCAACCAATCAGTCAGCCAGTTCCAAACAGGGC 3354
Qy 559 sProAsnGluLeuSerLeuGlyLeuGluAspLeuValIleProTrpThrAspLeuAspLe 579
Db 3355 AAATAGGGAACTTGGACTTGATGGTGTATATGGACATCCCGTGGTGTGATCTTAATAT 3414
Qy 579 uArgGluLysIleGlyAla----- 585
Db 3415 AAAAGAAAAGATTGGAGCAGGTAATAATTTACGGAAAAATTAATGATTCGGTCTAAAAA 3474
Qy 585 ----- 585
Db 3475 TGCAAAGAAATATGAATCTTTGAGGAAGTGGTTTTGCTTTGGACTCTGTTCTCGAACAA 3534
Qy 585 ----- 585
Db 3535 AATAAGGAAAAAGTGCCACCCATTTTGAGATTACATCTCTCTGTGTCCTTTAAATCTT 3594
Qy 586 -----GlySerPheGlyThrValTyrArgGlyGluT 596
Db 3595 CCACCTCTAAATTGAGCGACTGCTCTTTTCAGGTTCTTTGGCACCTGTCCACCGTGTGAGT 3654
Qy 596 ipHisGlySer----- 599
Db 3655 GGCATGGCTCGGTAAGAACTTTTTTGTGAGAAATTAGCGAGCTGAATTTTTTTTCGCTCT 3714
Qy 599 ----- 599
Db 3715 AAAAATTGGTTGTGACTTTTGGATCTGCTTGGTATTATAAAAGGCAAGTTATTGTATA 3774
Qy 599 ----- 599
Db 3775 TGTGACTCTCGTCTGTGACAGAAATTAACACCGGACAAAGGTGTCCCATTTTAGATGTA 3834
Qy 599 ----- 599
Db 3835 TATGTGCTTTATATCATAAATTTGTCTTCCGTGTTGAATTTTACAATCTATCACTAGA 3894
Qy 600 -----AspValAlaValL 604
Db 3895 AGAATTCATAATTTTGATTATTGCAGTAATATTCTCTATCAATTTTCAGGATGTTGCTGTGA 3954
Qy 604 ysIleLeuThrGluGlnAspPheHisProGluArgValAsnGluPheLeuArgGluVal- 623
Db 3955 AAATTCATGGAGCAAGACTTCCATGCTGAGCGTGTAAATGAGTTCTTTAAGAGAGGT-G 4013
Qy 623 ----- 623
Db 4014 CACAAATAAAATTTTCTCTTGATTTTGGTAATGAACCTTGTTGTATTATAATGTCCTCAAATGA 4073
Qy 624 -----AlaIleMetLysSerLeuArgHisProAsnIleValLeuP 637
Db 4074 TCTTGATTCGCTGTCAGGTTGCGATAATGAACGCCCTTCGCCACCCCTAACATTTGTTCTCT 4133
Qy 637 heMetGlyAlaValThrLysProProAsnLeuSerIleValThrGluTyrLeuSer---- 655
Db 4134 TCATGGTGGGTCACCTCAACCTCCAAATTTGTCAATAGTGACAGAATATTGTCTC-AAGG 4192
Qy 655 ----- 655
Db 4193 TACAATTACTTGGATTGGAAGGTTTGTGATGTAAGTGTAGATAATTTTGGCCTATAATGA 4252
Qy 656 -----ArgGlySerLeuTyrArgLeuLeuHisLysSerG 667
Db 4253 CTCTAATACCATGATTTCTTTCAAACAGAGGTAGTTTATACAGACTTTTGCATAAAAAGTG 4312
Qy 667 lyValLysAsp---IleAspGluThrArgArgIleAsnMetAlaPheAspVal----- 683

Db 4313 GAGCAAGGAGCAATTAGATGAGAGACGCTCGCCTGAGTATGGCTTATGATGTGGTATGTT 4372
Qy 683 ----- 683
Db 4373 TAACTCCTTATGTTACATGATGSGGTGATTACTTCTCTGATCTTGGTGTCTTTCACATGG 4432
Qy 684 -----AlaLysGlyMetAsnTyrLeuHisArgArgAsp 694
Db 4433 AACTTTCTTTCCAAATCTCTGTCACAGGCTAAGGGAATGAATATCTTCACAATCGCAAT 4492
Qy 695 ProProIleValHisArgAspLeuLysSerProAsnLeuValAspLysLysIleThr 714
Db 4493 CCTCCAATTGTGCATAGAGATCTAAATCTCCAAACTTATTGGTTGACAAAAAATATACA 4552
Qy 715 VallysVal----- 717
Db 4553 GTCAAGGT-TTGAATCTAAATTAGAAATTTGTGTGTCCAATGTTTGATTTTGATATTTT 4611
Qy 717 ----- 717
Db 4612 ATTCTCTTTGTGAGACAGCTTATATATAAATTATGATTTTAAATTCTAAATTTGGTTGG 4671
Qy 717 ----- 717
Db 4672 AGACATTACAAAAGGCGTTAATCTGCTGAAACTTAAAGATACAGCAGCCTCAAGCTGT 4731
Qy 717 ----- 717
Db 4732 CGTCTTAAAAACAATCAGAACATTATTATTCTAACTCCTCAATTTGTCTTGAATTTTCAG 4791
Qy 718 ---CysAspPheGlyLeuSerArgLeuLysAlaArgThrPheLeuSerSerLysSerAla 736
Db 4792 GTTTGTGAATTTGGTCTCTCGGATTGAAGGCCAGCACGTTTCTTCTCGAAGTCAGCA 4851
Qy 737 AlaGlyThr----- 739
Db 4852 GCTGGAACCGTAAGTTCAGTTTGTGTTTGAACCTTAAACACGCTGAACAACGTAACCTTCTT 4911
Qy 740 -----ProGluTr 742
Db 4912 CTAGGTCCTATTTCCAAATGGAAGCTAAATAATTACTGACTTTTGATATATCAGCCCGAGTG 4971
Qy 742 pMetAlaProGluValLeuArgAspGluProSerAsnGluLysSerAspValTyrSerPh 762
Db 4972 GATGGCACCAAGTCTCTCGAGATGAGCCGCTCTAATGAAAAGTCAGATGTGTACAGCTT 5031
Qy 762 eGlyValIleLeuTrpGluLeuAlaThrLeuGlnGlnProTrpCysAsnLeuAsnProAl 782
Db 5032 CGGGGTCACTCTTGTGGAGCTTGTACATTGCAACCAACCATGGGGTAACTTAAATCCGGC 5091
Qy 782 aGln----- 783
Db 5092 TCAGGTACTTCCCACTCTAAACATCCCAATAATAATGATATTATTTTGTGATTGGAAGT 5151
Qy 784 -----Va 784
Db 5152 CCCTCACTCTACATTTTATAACATGCTATATATGATCATCCAACAAAATGTTCCATAGGT 5211
Qy 784 lValAlaAlaValGlyPheLysGlyLysArgLeuAspIleProArgAspValAsnProLy 804
Db 5212 TGTAGCTGCGGTTGGTTTCAAGTGTAAACGGCTGGAGATCCCGCGTAACTCTGAATCCTCA 5271
Qy 804 sLeuAlaSerLeuIleValAlaCysTrpAla----- 814
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Qy 815 -----AspGluProTr 818
Db 5331 TTGAATTTCTTTGAATAGACTTTCATGTTTATGATGTGTTTATGATGTGTTTCCATGAGCCATG 5390
Qy 818 pLysArgProSerPheSerIleMetGluThrLeuLysProMetThrLysGlnAlaPr 838
Db 5391 GAAGCGTCCATCATTTGCAACTATATATGACTTGTCTAAGACCATGATCAAAATCAGCGT 5450

QY 838 oProGlnGlnSerArgThrAsp 845
Db 5451 TCCTCCGCCCAACCGCTCGGAT 5472

RESULT 15
US-07-928-464-5
; Sequence 5, Application US/07928464
; Patent No. 5367065
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene and
; TITLE OF INVENTION: Mutations
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
; ADDRESSEE: No. 5367065ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/928,464
; FILING DATE: 19920810
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Suzanne E.
; REGISTRATION NUMBER: 32,279
; REFERENCE/DOCKET NUMBER: UPN-1086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5890 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-928-464-5

Alignment Scores:
Pred. No.: 1.03e-201 Length: 5890
Score: 2063.00 Matches: 555
Percent Similarity: 41.77% Conservative: 110
Best Local Similarity: 34.86% Mismatches: 160
Query Match: 46.52% Indels: 772
DB: 1 Gaps: 34

US-09-904-389-2 (1-850) x US-07-928-464-5 (1-5890)

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QY 21 ValGly-----ThrGlyAlaSerThrSerPheTyrAspSerValAlaAla----- 35
Db 414 GTGTCAAGTTTCCGTACCGGAGCTCCTCCGCTCACTATGATTCCTTGTCTGAGCGGAAAC 473
QY 36 -----GlyGlyAsnValIleLysGlyArgThrAspArg---ValPheAsp 49
Db 474 AGGAGCAACCATACACGCGGGAACACCCGCGGAAAGCTAAGCGCGAGAGAGCGGATTTGAT 533
QY 50 TrpAsp-----GlySerGlyAspHisArgLeuAsnThrGlnAlaTyrArgIle 65
Db 534 TGGATCCTAGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 593

QY 66 Gly---AsnLeuTyr---SerTrpIleGlyLeuGlnArgHisSerSerGlySerSerTyr 83
Db 594 GGGAAATAATATGATGCTTCGCTCTAGGGTTGCAAAAGSCAATCCAGTGGGAGTAGTTTC 653
QY 84 AspAspSerSerLeuSerSerAspTyrTyrAlaProThrLeuSerAsnProAlaAlaAsn 103
Db 654 GGTGAGAGCTCTTTGTTCTGGGGATTATTACATGCCTACGCTTTCT---GCGGCGGCTAAC 710
QY 104 GluIleAsnAlaLeuGluTyrIleLeuAspAspPheArgVal----- 118
Db 711 GAGATCGAATCTGTTGGATTTCCTCAAGATGATGGGTTTAGCTTGGATTGGTGGTGGT 770
QY 119 -----MetLysAlaValGlySerGlyGly---SerSerGlyLys 130
Db 771 GGAGGAGATTTCAGGATACAGATGGCGCGGACTCCGCTGGAGGGTCTTCATCTGGGAAG 830
QY 131 SerTrpAlaGlnGlnThrGluSerPheGlnLeuGlnGlnProLeuValLeuArgLeu 150
Db 831 AGCTGGCGCAGCAGACGAGGAGAGATTATCAGCTGCAGCTTGCATTTGGCGTTAAGGCTT 890
QY 151 SerSerAsp***ThrCysAlaAspAspProAsnPheMetAspProIleProAspGluAla 170
Db 891 TCGTCGGAGGCTACTTGTCCGACGATCCGAACCTTCTGGATCCTGTACCGGACGAGTCT 950
QY 171 AlaLeuArgSerLeuSerIleSerAlaGluAlaIleSerHisArgPheTrp----- 187
Db 951 GCTTTACGGACTTCGCCAAGTTTCAGCCGAAACCGTTTTCACATCGTTTCTGGGTATTGTT 1010
QY 187 ----- 187
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QY 187 ----- 187
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QY 188 -----ValAsnGlyCysMe 192
Db 1131 TGTTTAGATACATTGCAGAGTATGATTGTTTGTGTGTCATCAGGTTAATGGCTGCTT 1190
QY 192 tSerTyrLeuGluLysValProAspGlyPheTyrLeuIleHisGlyMetAspProTyrVa 212
Db 1191 ATCGTACTATGATAAAGTTCTGTATGGGTTTATATGATGAATGCTCTGGATCCCTATAT 1250
QY 212 lTrpSerLeuCysThrAsnLeuGlnGluAspGlyArgIleProSerPheGluSerLeuLy 232
Db 1251 TTGGACCTTATGCATCGACCTGCATGAAAGTGGTGCATCCCTTCAATTGAATCATTAAAG 1310
QY 232 sThrValAspSerSerIleGlySerSerIleGluValValLeuIleAspArgHisSerAs 252
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QY 252 pAlaSerLeuLysGluLeuGlnAsnArgValHisAsnIleSerSerSerCysValThrTh 272
Db 1371 TCCAGCCTTCAAGGAACTTCACAATAGAGTCCACGACATATCTTGTAGCTGCATTACCAC 1430
QY 272 rLysGluValAlaAspHisIleAlaLysLeuValCysAsnHisLeuGly----- 288
Db 1431 AAAAGAGGTTGTTGATCAGCTGGCAAAGCTTATCTGCAATCGTATGGGTTTGTACTCAT 1490
QY 288 ----- 288
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QY 320 euCysSerLeuSerValGlyLeuCysArgHisArgAlaLeuLeuPhe-Lys----- 336

QY 656 -----ArgGlySerLeuTyrArgLeuLeuHisLysSerG 667
Db 3831 CTCTAATAACCATGATTTCTTTCAAAACAGAGGTAGTTTATACAGACTTTTGCAATAAAAGTG 3890
QY 667 lyValLysAsp---IleAspGluThrArgArgIleAsnMetAlaPheAspVal----- 683
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Db 4011 AACTTTCTTTCCAAATTCCTGTGCACAGGCTAAGGGAATGAATTATCTTCACAAATCGCAAT 4070
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QY 740 -----ProGluTr 742
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QY 784 -----Va 784
Db 4730 CCCTCACTCTACATTTTATAACATGCTATATATGATCATCCAAACAAAATGTTCCATAGGT 4789
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Db 4850 GGTTCAGCCCATPAATCGAGGGTTGTTGGAC-CAAGTACGTTAAGATTTTCTATCTCTTTT 4908

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QY 818 plysArgProSerPheSerSerIleMetGluThrLeuLysProMetThrLysGlnAlaPr 838
Db 4969 GAAGCGTCCATCATTGCAACTATAATGGACTTGCTAAGACCATGATCAAATCAGCGGT 5028
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Search completed: October 24, 2003, 03:01:04
Job time : 272 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2003, 02:51:03 ; Search time 942 Seconds
(without alignments)
2419.884 Million cell updates/sec

Title: US-09-904-389-2
Perfect score: 4435
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:*

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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description	
					Query	ID
1	4433	100.0	3286	10	US-09-904-389-1	Sequence 1, Appli

2	2742.5	61.8	2466	12	US-10-171-404A-47	Sequence 47, Appli
3	1538	34.7	2892	10	US-09-938-842A-1073	Sequence 1073, Ap
4	1193	26.9	2661	10	US-09-938-842A-1085	Sequence 1085, Ap
5	806	18.2	2211	10	US-09-938-842A-1577	Sequence 1577, Ap
6	588	13.3	1662	10	US-09-938-842A-1014	Sequence 1014, Ap
7	513	11.6	1638	10	US-09-938-842A-903	Sequence 903, App
8	507	11.4	1063	14	US-10-106-698-2068	Sequence 2068, Ap
9	504.5	11.4	1365	9	US-09-757-982-6	Sequence 6, Appli
10	504.5	11.4	2120	9	US-09-757-982-4	Sequence 4, Appli
11	475.5	10.7	2719	10	US-09-917-800A-1405	Sequence 1405, Ap
12	469.5	10.6	2229	12	US-10-440-341-6	Sequence 6, Appli
13	469.5	10.6	2510	14	US-10-057-550-89	Sequence 89, Appli
14	469.5	10.6	2510	14	US-10-173-225B-67	Sequence 67, Appli
15	466.5	10.5	3435	12	US-10-210-120-86	Sequence 86, Appli
16	466.5	10.5	3454	10	US-09-969-347-226	Sequence 226, App
17	466.5	10.5	3454	14	US-10-171-581-312	Sequence 312, App
18	457.5	10.3	1627	9	US-09-828-313-16	Sequence 16, Appli
19	457.5	10.3	2975	12	US-10-440-341-2	Sequence 2, Appli
20	457.5	10.3	2977	10	US-09-969-347-207	Sequence 207, App
21	457.5	10.3	2977	12	US-10-371-138-1	Sequence 1, Appli
22	457.5	10.3	2977	14	US-10-057-550-25	Sequence 25, Appli
23	457.5	10.3	2977	14	US-10-173-225B-64	Sequence 64, Appli
24	453	10.2	3393	12	US-10-263-480-1	Sequence 1, Appli
25	453	10.2	5527	10	US-09-880-107-3710	Sequence 3710, Ap
26	452	10.2	3840	12	US-10-204-041-3	Sequence 3, Appli
27	450.5	10.2	1428	10	US-09-938-842A-882	Sequence 882, App
28	445.5	10.0	4705	12	US-10-312-918-1	Sequence 1, Appli
29	445.5	10.0	4786	12	US-10-312-918-3	Sequence 3, Appli
30	445	10.0	2440	14	US-10-153-668-435	Sequence 435, App
31	445	10.0	3428	14	US-10-153-668-437	Sequence 437, App
32	444.5	10.0	3365	14	US-10-153-668-323	Sequence 323, App
33	444.5	10.0	3761	12	US-09-814-353-20138	Sequence 20138, A
34	444.5	10.0	6378	12	US-10-252-157-482	Sequence 482, App
35	440	9.9	3558	13	US-10-143-133-1	Sequence 1, Appli
36	438	9.9	3111	13	US-10-014-882-1	Sequence 1, Appli
37	438	9.9	3518	13	US-10-014-882-3	Sequence 3, Appli
38	438	9.9	5549	12	US-10-354-358-23	Sequence 23, Appli
39	432	9.7	2449	14	US-10-220-801-11	Sequence 11, Appli
40	432	9.7	2456	12	US-10-021-660-41	Sequence 41, Appli
41	432	9.7	2456	13	US-10-186-399-1	Sequence 1, Appli
42	432	9.7	2500	9	US-09-977-269-3	Sequence 3, Appli
43	432	9.7	2500	10	US-09-977-260-3	Sequence 3, Appli
44	432	9.7	2500	11	US-09-977-261-3	Sequence 3, Appli
45	430.5	9.7	2604	14	US-10-171-581-317	Sequence 317, App

ALIGNMENTS

RESULT 1
US-09-904-389-1
; Sequence 1, Application US/09904389
; Patent No. US20020129404A1
; GENERAL INFORMATION:
; APPLICANT: Clendennen, Stephanie K.
; APPLICANT: Schuster, Debra K.
; TITLE OF INVENTION: CTRL HOMOLOGUE FROM MELON
; FILE REFERENCE: 4257-0029.30
; CURRENT APPLICATION NUMBER: US/09/904,389
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 60/218,307
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3286
; TYPE: DNA
; ORGANISM: Cucumis melo
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (81)...(81)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (593)...(594)

OTHER INFORMATION: n = A,T,C or G
US-09-904-389-1

Alignment Scores:
Pred. No.: 0
Score: 4433.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 99.95%
DB: 10

Length: 3286
Matches: 850
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-904-389-2 (1-850) x US-09-904-389-1 (1-3286)

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DB 253 AAAGGAGAACCGATAGGTTTTTGTGATTGGGATGGAGTGGTGATCACAGGTAAACACG 312
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QY 81 SerSerTyrAspAspSerSerLeuSerSerAspTyrTyrAlaProThrLeuSerAsnPro 100
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QY 121 AlaValGlySerGlyGlySerSerGlyLysSerTrpAlaGlnGlnThrGluGluSerPhe 140
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DB 1093 TGCAGCTTATCTGTGGCTTTTGTAGACATCGTGTCTCTTTTANTCAAAGTCTCTAGCTGAT 1152
QY 341 SerIleAspLeuProCysArgIleAlaLysGlyCysLysTyrCysThrArgAspAla 360
DB 1153 TCAATTGATTTACCTGTGCAATTGCCAAAGGATGTAATATTGCACCTAGAGATGATGCT 1212
QY 361 SerSerCysLeuValArgPheGlyLeuAspArgGluTyrLeuIleAspLeuIleGlyArg 380
DB 1213 TCATCTTGCCTTGTAGGTTTCGGGCTTGATAGGAATATCTCATCGATCTGATTGGGAGG 1272
QY 381 ProGlyCysLeuCysGlnProAspSerLeuLeuAsnGlyProSerSerIleSerIleSer 400
DB 1273 CCAGGTTGCTTATGCCAACCTGATTTCTTTGCTCAATGGTCCATCATCTCAATTTCT 1332
QY 401 SerProLeuArgPheProArgLeuLysProIleGluSerThrIleAspPheArgSerLeu 420
DB 1333 TCACCATTCGATTTCCAAGACTAAACCTATTGAATCTACCAATTGATTTCAAGTCACTG 1392
QY 421 AlaLysGlnTyrPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAlaSerSer 440
DB 1393 GCCAAACAGTATTTCTGGATAGCCAATCACTTAATCTTGTATTGATGAAGCTTCTTTCA 1452
QY 441 GlyAsnValValSerGlyLysAspAlaAlaPheSerValTyrGlnArgProLeuAsnArg 460
DB 1453 GGTAATGTTGATCTCGGAAGGATGCTGCATTTCTCGTCTATCAAAGGCCATTAATAGG 1512
QY 461 LysAspValAspGlyLysThrIleValValThrGlyAspLysAspArgAsnSerGlnLeu 480
DB 1513 AAGGATGTAGATGGAAAAACCATAGTGGTTACTGTGTGACAAGGACAGAAATTTCAAGTTA 1572
QY 481 LeuAsnLysLysAlaAlaGlnLeuAsnThrGlnAspGlyLysSerGluGlnPheArgSer 500
DB 1573 TTAAATAAAAAAGCAGCCCACTGAATACTCAAGATGGAAAGTCTGAGCAATTTAGATCA 1632
QY 501 CysValAlaSerProTyrSerValGlnSerThrProPheValGluAsnValValProLeu 520
DB 1633 TGTGTTGCTTCTCCATATAGTGTACAGTCGACCCCTTTGTAGAAAATGTAGTCCCTTTA 1692
QY 521 SerHisIleSerHisIleGlySerGluAspSerGluHisLeuLeuAlaLeuSerHisPro 540
DB 1693 AGCCATATCTCACACATTTGGTTCTGAAGATTTCGAGCATCTCTTAGCATTTGCTCATCCA 1752
QY 541 ArgMetAspHisValAsnAsnLeuPropheValHisGlySerGlnLeuIleArgLysPro 560
DB 1753 AGGATGGATCATGTTTAACAATTTACCATTTGTTTCATGTGTAGTCAGTTGATTAGAAAAACCA 1812
QY 561 AsnGluLeuSerLeuGlyLeuGluAspLeuValIleProTrpThrAspLeuAspLeuArg 580
DB 1813 AATGAGCTTTCCCTTGGCTTAGAAGATTTGGTTATTTCCATGGACAGATCTTGAATTGAGG 1872
QY 581 GluLysIleGlyAlaGlySerPheGlyThrValTyrArgGlyGluTrpHisGlySerAsp 600
DB 1873 GAGAAAAATTGGACGAGGTTCTTTTGGGACTGTATATCGTGTGAGTGGCATGGCTCTGAT 1932
QY 601 ValAlaValLysIleLeuThrGluGlnAspPheHisProGluArgValAsnGluPheLeu 620
DB 1933 GTTGCTGTGAAGATCTTCACAGAACACAGACTTCCATCTCTGAACGTGTTAATGAGTTTCTG 1992
QY 621 ArgGluValAlaIleMetLysSerLeuArgHisProAsnIleValLeuPheMetGlyAla 640
DB 1993 AGAGAGGTTGCTATCATGAATCTTTTACGACATCTTAATATTGTACTGTTTATGGGTGCG 2052
QY 641 ValThrLysProProAsnLeuSerIleValThrGluTyrLeuSerArgGlySerLeuTyr 660
DB 2053 GTGACCAAGCCCAAACTTGTCCATTGTCCCGAATATCTATCGAGAGGTAGCTTGTAT 2112
QY 661 ArgLeuLeuHisLysSerGlyValLysAspLeAspGluThrArgArgIleAsnMetAla 680

Db 2113 AGGCTTTGTCATAGTCAGGTGTCAAAGACATAGATGAAACACGTCGAATAAATATGGCT 2172
Qy 681 PheAspValAlaLysGlyMetAsnTyrLeuHisArgArgAspProProileValHisArg 700
Db 2173 TTTGATGTGGCAAAGGGAATGAACACTACCTCCACAGACGTGATCCTCCAATTTGTTCAATCGT 2232
Qy 701 AspleuLysSerProAsnLeuLeuValAspLysLysTyrThrValLysValCysAspPhe 720
Db 2233 GATTAAAAATCACCGAATCTGTAGTTGACAAAGATATACAGTCAAGGTTGTGATTTT 2292
Qy 721 GlyLeuSerArgLeuLysAlaArgThrPheLeuSerSerLysSerAlaAlaGlyThrPro 740
Db 2293 GGTCCTCCCGTTTAAAGGCACGCACATTTCTTTTCATCCAAATCTGCAGCTGGAACACCT 2352
Qy 741 GluTrpMetAlaProGluValLeuArgAspGluProSerAsnGluLysSerAspValTyr 760
Db 2353 GAATGGATGGCACCAAGACTACTACCGGATGAACCATCAAAATGAAAGTCAGATGTTTAC 2412
Qy 761 SerPheGlyValIleLeuTrpGluLeuAlaThrLeuGlnGlnProTrpCysAsnLeuAsn 780
Db 2413 AGCTTTGGAGTGATTTTGTGGAGTTGGCAACTTTGCAACAGCCATGGTGTAAATCTAAAC 2472
Qy 781 ProAlaGlnValAlaAlaValGlyPheLysGlyLysArgLeuAspIleProArgAsp 800
Db 2473 CCAGCTCAGGTTGTCCAGCTGTGGATTTAAGGGCAAAAGGCTTGACATCCACGCTGAT 2532
Qy 801 ValAsnProLysLeuAlaSerLeuIleValAlaCysTrpAlaAspGluProTrpLysArg 820
Db 2533 GTAAATCCCAAAATGGCTTCCCTTAATAGTGGCTTGGCCCGATGAGCCATGGAAACGT 2592
Qy 821 ProSerPheSerSerIleMetGluThrLeuLysProMetThrLysGlnAlaProProGln 840
Db 2593 CCTTCTTTTCCAGCATTTATGGAAACCTTGAAACCAATGACTAAACAAGCCACCTCAA 2652
Qy 841 GlnSerArgThrAspThrLeuSerValMet 850
Db 2653 CAAAGTCGACAGACACCCCTCTCGGTTATG 2682

RESULT 2

US-10-171-404A-47
; Sequence 47, Application US/10171404A
; Publication No. US20030177529A1
; GENERAL INFORMATION:
; APPLICANT: BASF PLANT SCIENCE GMBH
; TITLE OF INVENTION: SUGAR AND LIPID METABOLISM REGULATORS IN PLANTS II
; FILE REFERENCE: 16313-0119
; CURRENT APPLICATION NUMBER: US/10/171,404A
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/295,680
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 47
; LENGTH: 2466
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-171-404A-47

Alignment Scores:
Pred. No.: 7.68e-284 Length: 2466
Score: 2742.50 Matches: 546
Percent Similarity: 73.63% Conservative: 99
Best Local Similarity: 62.33% Mismatches: 144
Query Match: 61.84% Indels: 87
DB: 12 Gaps: 14

US-09-904-389-2 (1-850) x US-10-171-404A-47 (1-2466)

Qy 1 MetGluMetProGlyArgArgSerAspTyrSerLeuLeuSerGlnIleProAspGluGlu 20
Db 1 ATGGAAATGCCCGGTAGAAGATCTAATTACACTTTCCTTAGTCAATTTTCTGACGATCAG 60

Qy 21 ValGly-----ThrGlyAlaSerThrSerPheTyrAspSerValAlaAala----- 35
Db 61 GTGTCACTTTCGGTCACCGGAGCTCCTCCGCCTCCTATGATTCCTTGTCCAGCGAAAC 120
Qy 36 -----GlyGlyAsnValIleLysGlyArgThrAspArg--ValPheAsp 49
Db 121 AGGAGCAACCAATAACAGCGGGAACACCGGAAAGCTAAGCGGAGAGAGGGGGATTGTAT 180
Qy 50 TrpAsp-----GlySerGlyAspHisArgLeuAsnThrGlnAlaTyrArgIle 65
Db 181 TGGGATCCTAGCGGTGGTGGTGGTGATCATAGCTTGAATAATCAACCGAATCGGGTT 240
Qy 66 Gly---AsnLeuTyr---SerTrpIleGlyLeuGlnArgHisSerSerGlySerSerTyr 83
Db 241 GGGAAATAATATGATGCTTCGTCTCTAGGGTTGCAAGGCAATCCAGTGGGAGTAGTTTC 300
Qy 84 AspAspSerSerLeuSerSerAspTyrTyrAlaProThrLeuSerAsnProAlaAalaAsn 103
Db 301 GGTGAGAGCTCTTTGTCTGGGGATTATTACATGCTTACGCTTCT--GCGCGGCTAAC 357
Qy 104 GluIleAsnAlaLeuGluTyrIleLeuAspAspAspPheArgVal----- 118
Db 358 GAGATCGAATCTGTTGGATTTCCTCAAGATGATGGGTTAGGCTTGGATTGGTGGTGGT 417
Qy 119 -----MetLysAlaValGlySerGlyGly---SerSerGlyLys 130
Db 418 GGAGGAGATTGAGGATACAGATGGCGGCGGACTCCGCTGGAGGCTCTTCACTCTGGAAAG 477
Qy 131 SerTrpAlaGlnGlnThrGluGluSerPheGlnLeuGlnProLeuValLeuArgLeu 150
Db 478 AGCTGGCGCAGCAGACGGAGGAGAGTTATCAGCTGCAGCTTGCAATTGGCGTTAAGGCTT 537
Qy 151 SerSerAsp**ThrCysAlaAspAspProAsnPheMetAspProIleProAspGluAla 170
Db 538 TCGTCGGAGGCTACTTGTGCCGACGATCCGAACTTTCTGGATCCTGTACCGGACGAGTCT 597
Qy 171 AlaLeuArgSerLeuSerIleSerAlaGluAlaIleSerHisArgPheTrpValAsnGly 190
Db 598 GCTTTACGGACTTCGCCAAGTTTCAGCCGAAACCGTTTCACATCGTTTCTGGGTTAATGGC 657
Qy 191 CysMetSerTyrLeuGluLysValProAspGlyPheTyrLeuIleHisGlyMetAspPro 210
Db 658 TGCTTATCGTACTATGATAAAGTTCTCTGATGGGTTTTATATGATGAATGGTCTGGATCCC 717
Qy 211 TyrValTrpSerLeuCysThrAsnLeuGlnGluAspGlyArgIleProSerPheGluSer 230
Db 718 TATATTTGGACCTTATGCATCGACCTGCATGAAAGTGTCGCATCCCTTCAATTGAATCA 777
Qy 231 LeuLysThrValAspSerSerIleGlySerSerIleGluValValLeuIleAspArgHis 250
Db 778 TTAAGAGCTGTTGATTTCTGGTGTGATTCTTCGCTTGAAGCGCATCATAGTTGATAGCGCT 837
Qy 251 SerAspAlaSerLeuLysGluLeuGlnAsnArgValHisAsnIleSerSerSerCysVal 270
Db 838 AGTGATCCAGCCTTCAAGGAACCTTCAATAAGATAGAGTCCACGACATATCTTGTAGCTGCATT 897
Qy 271 ThrThrLysGluValAlaAspHisIleAlaLysLeuValCysAsnHisLeuGlyGlySer 290
Db 898 ACCACAAAGAGGTTGTGATCAGCTGGCAAAAGCTTATCTGCAATCGTATGGGGGTCCA 957
Qy 291 ValSerGluGlyGluAspAspLeuValSerAlaTrpLysGluCysSerAspLeuLys 310
Db 958 GTTATCATGGGGGAAGATGAGTTGGTTCCCATGTGGAAGGAGTGCATTGATGGTCTAAAAA 1017
Qy 311 GluCysLeuGlySerAlaValIleProLeuCysSerLeuSerValGlyLeuCysArgHis 330
Db 1018 GAA---ATCTTTAAAGTGGTGGTTCCCATAGGTAGCCTCTCTCTGTGGACTCTGCAGACAT 1074
Qy 331 ArgAlaLeuLeuPheLysValLeuAlaAspSerIleAspLeuProCysArgIleAlaLys 350
Db 1075 CGAGCTTTACTCTTCAAGTACTGGCTGCACATAATTGATTTTACCTGTGCAATTGCCAAA 1134
Qy 351 GlyCysLysTyrCysThrArgAspAspAlaSerSerCysLeuValArgPheGlyLeuAsp 370


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Db 1135 GGATGTAATAATGTAATAGAGACGATCGCTTCGTGCTTGTTCAGGTTGGGCTTGAT 1194
QY 371 ArgGluTyrLeuLeuAspLeuLeuGlyArgProGlyCysLeuCysGlnProAspSerLeu 390
Db 1195 AGGAGTACCTGGTGTATTTAGTAGGAAAGCCAGGCTACTTATGGAGCCTGATTCCTTG 1254
QY 391 LeuAsnGlyProSerSerIleSerSerProLeuArgPheProArgLeuLysPro 410
Db 1255 CTAAATGGTCTTCATCTATCTCAATTTCTTCTCTCTGCGGTTTCCACGACCAAGCCA 1314
QY 411 IleGluSerThrIleAspPheArgSerLeuAlaLysGlnTyrPheLeuAspSerGlnSer 430
Db 1315 GTTGAACCCGCGAGTGGATTTAGGTACTAGCCAAACAATATTTCTCCGATAGCCAGTCT 1374
QY 431 LeuAsnLeuValPheAspGluAlaSerSerGlyAsnValValSerGlyLysAspAlaAla 450
Db 1375 CTAAATCTGTTTTCGATCTCTGATCCTGATCAGAT-----GATATGGGA 1413
QY 451 PheSerValTyrGlnArgProLeuAsnArgLysAspValAspGlyLysThrIleValVal 470
Db 1414 TTCTCAATGTTTCATAGGCAATATGATAATCCGGGTGAGAGAAATGACCGATGGCAGAA 1473
QY 471 ThrGlyAspLysArgAsnSerGlnLeuLeuAsnLysLysAlaAlaGlnLeuAsnThr 490
Db 1474 AATGGTGGT----- 1482
QY 491 GlnAspGlyLysSerGluGlnPheArgSerCysValAlaSerProTyrSerValGlnSer 510
Db 1483 -----GGGTCT 1488
QY 511 ThrProPheValGluAsnValValProLeuSerHisIleSerHisIleGlySerGluAsp 530
Db 1489 TTGCCACCCAGTGCTAATATGCTCTCA----- 1515
QY 531 SerGluHisLeuLeuAlaLeuSerHisProArgMetAspHisValAsnAsnLeuProPhe 550
Db 1516 ---CAGAACATGATCGTGGTCAATCAATGAAGCAGCACCTATGATGCCCCACCA 1572
QY 551 ValHisGlySerGlnLeuLeuIleArgLysProAsnGluLeuSerLeuGlyLeuGluAspLeu 570
Db 1573 ATCAGTCAGCCAGTTCACAAACAGGGCAATAGGGAACITGGACTTGATGGTGTATGATG 1632
QY 571 ValIleProTyrThrAspLeuAspLeuArgGluLysIleGlyAlaGlySerPheGlyThr 590
Db 1633 GACATCCCGTGGTGTGATCTTAATAAAGAAAGAAAGATTGGAGCAGGTTCTTGGCACT 1692
QY 591 ValTyrArgGlyGluTyrHisGlySerAspValAlaValLysIleLeuThrGluGlnAsp 610
Db 1693 GTCCACCGTGTGATGGCATGGCTCGATGTTGCTGTGAAAATTTCTCATGGAGCAAGAC 1752
QY 611 PheHisProGluArgValAsnGluPheLeuArgGluValAlaIleMetLysSerLeuArg 630
Db 1753 TTCCATGCTGAGCGGTGTAATGAGTTCTTAAGAGAGGTTGCGATAATGAAACGCTTCGC 1812
QY 631 HisProAsnIleValLeuPheMetGlyAlaValThrLysProProAsnLeuSerIleVal 650
Db 1813 CACCCTAACATTTGTTCTTCTCATGGGTGCGGTCACTCAACCTCCAAATTTGTCATAGTG 1872
QY 651 ThrGluTyrLeuSerArgGlySerLeuTyrArgLeuLeuHisLysSerGlyValLysAsp 670
Db 1873 ACAGAAATTTGTCAAGAGGTAGTTTATACAGACTTTTGCATAAAGTGGAGCAAGGGAG 1932
QY 671 ---IleAspGluThrArgArgIleAsnMetAlaPheAspValAlaLysGlyMetAsnTyr 689
Db 1933 CAATTAGATGAGAGAGCTCGCCTGATGCTTATGATGGCTTATGATGGCTAAGGGAATGATAT 1992
QY 690 LeuHisArgAspProIleValHisArgAspLeuLysSerProAsnLeuVal 709
Db 1993 CTTCACAATCGCAATCTCCAATTTGTCATAGAGATCTAAAATCTCCAACTATTGGTT 2052
QY 710 AspLysLysTyrThrValLysValCysAspPheGlyLeuSerArgLeuLysAlaArgThr 729
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Db 2053 GACAAAAAATATACAGTCAAGGTTTGTGATTTTGGTCTCTCGCGATTGAAGGCCAGCAG 2112
QY 730 PheLeuSerSerLysSerAlaAlaGlyThrProGluTyrMetAlaProGluValLeuArg 749
Db 2113 TTTCTTTCTCGAAGTCAGCAGCTGGAACCCCGAGTGGATGGCACCAGAGTCTCTCGGA 2172
QY 750 AspGluProSerAsnGluLysSerAspValTyrSerPheGlyValIleLeuTyrGluLeu 769
Db 2173 GATGAGCGGTCTAATGAAAAAGTCAGATGTGTACAGCTTCGGGGTCACTTTGTGGAGCTT 2232
QY 770 AlaThrLeuGlnGlnProTyrCysAsnLeuAsnProAlaGlnValValAlaAlaValGly 789
Db 2233 GCTACATTCGAACAACCATGGGTAACTTAAATCCGGCTCAGGTGTAGTGCAGTGGT 2292
QY 790 PheLysGlyLysArgLeuAspIleProArgAspValAsnProLysLeuAlaSerLeuIle 809
Db 2293 TTCAAGTGTAAACGGCTGGAGATCCCGGTAATCTGAATCTCAGGTTGCAGCCATAATC 2352
QY 810 ValAlaCysTyrAlaAspGluProTyrLysArgProSerPheSerSerIleMetGluThr 829
Db 2353 GAGGTTGTTGGACCAATGAGCCATGGAAGCGTCCATCATCTTGAACATAATATGAGACTTG 2412
QY 830 LeuLysProMetThrLysGlnAlaProProGlnGlnSerArgThrAsp 845
Db 2413 CTAAGACCATGATCAAAATCAGCGGTTCTCCGCCCAACCGCTCGGAT 2460
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RESULT 3

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US-09-938-842A-1073
; Sequence 1073, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krebs, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2000-08-24
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1073
; LENGTH: 2892
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1073
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Alignment Scores:
Pred. No.: 2.2e-154 Length: 2892
Score: 1538.00 Matches: 367
Percent Similarity: 54.94% Conservative: 128
Best Local Similarity: 40.73% Mismatches: 253
Query Match: 34.68% Indels: 154
DB: 10 Gaps: 23
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US-09-904-389-2 (1-850) x US-09-938-842A-1073 (1-2892)

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QY 4 ProGlyArgArgSerAspTyr---SerLeuLeuSerGlnIleProAspGluValGly 22
Db 398 CCGATGAGGAGAGAGAGAGCTTCTGTGTTCTTCTCCGGCTGATCCCGCT-CCGCTTCTGCT 456
QY 23 ThrGlyAlaSerThrSerPheTyrAspSerValAlaAlaGlyGlyAsnValIleLysGly 42
Db 457 ACTTCTTCGCGGATTCTATCATTTGATTCG---GCTAGGACGGTTAATCATATGAAACGA 513
QY 43 ArgThrAspArgValPheAspTyrAspGlySerGlyAspHisArgLeuAsnThrGlnAla 62
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Db 514 AACATTGATCGGAGCTTTGACAGAGAGGTTTCGCTTCCC---CGAATGTCGAGTGAGAGC 570
QY 63 TyrArgIleGlyAsnLeuTyrSerTrpIleGlyLeuGlnArgHisSerSerGlySerSer 82
Db 571 AGCTTCGCTGGAAGCTTCTTC-----TCCGGGACGAGC 603
QY 83 TyrAspAsp-----SerSerLeuSerSerAspTyrTyrAlaProThrLeuSerAsnPro 100
Db 604 GTGGACGGGAATTCTCCAAATTTCTCAAGTCATACAGACGCAAGGAAACTTCGACCACC 663
QY 101 AlaAlaAsnGluIleAsnAlaLeuGluTyrIleLeuAspAspAspPheArgValMetLys 120
Db 664 ACGCTTGCTCAGTGAACAAAGAGGAA-----GAAGAAGTTGAGGTTAGGGAA 711
QY 121 AlaValGlySerGlyGlySerSerGlyLys-----SerTrpAlaGlnGlnThrGluGlu 138
Db 712 -----CAGGGCAAGAGAGCAAGCTTAGCGCAGAGTCAAGAGAA 750
QY 139 SerPheGlnLeuGlnGlnProLeuValLeuArgLeuSerSerAsp**ThrCysAlaAsp 158
Db 751 GGCTATTACTGCAGGTTCACGCTTGCTAAGTGGCTAAGTCTCAAGCA----- 798
QY 159 AspProAsnPheMetAspProIleProAspGluAlaAlaLeuArgSerLeuSerIle--- 177
Db 799 -----AACCTAGCATGTGAGTCTGTTTCATATACAG 828
QY 178 SerAlaGluAlaIleSerHisArgPheTrpValAsnGlyCysMetSerTyrLeuGluLys 197
Db 829 AGCACAGAATCTATCTCTACCGTTTGGGTAAAGTGGTGTGTTTATCATACAGTGACAAG 888
QY 198 ValProAspGlyPheTyrLeuIleHisGlyMetAspProTyrValTrpSerLeuCysThr 217
Db 889 ATATCAGATGGATTTTACAGTATATTAGGAATGGATCCGPATCTTTGGTTGATGTGAAC 948
QY 218 AsnLeuGlnGluAspGlyArgIleProSerPheGluSerLeuLysThrValAspSerSer 237
Db 949 AATTCTGAGGATGGCAACGAATTCATCTCTTTTGTACTCAAGGAGACTGAGCCGAAT 1008
QY 238 IleGlySerSerIleGluValValLeuIleAspArgHisSerAspAlaSerLeuLysGlu 257
Db 1009 ---GATACATCAATGAAGTGGTTTGTATAGATAGACGTGAGGACTCACGCTCTAAAGAA 1065
QY 258 LeuGlnAsnArgValHisAsnIleSerSerSerCysValThrThrLysGluValAlaAsp 277
Db 1066 CTGGAGGATAAGSCACATGAGCTGTATTGTTCTTCAGACAAACATGTTAGTGCTCGTCGAG 1125
QY 278 HisIleAlaLysLeuValCysAsnHisLeuGlyGlySerValSerGluGlyGluAspAsp 297
Db 1126 AAACCTGGCAGACTGTTGCGGTCTATATGGGGGGAATTTCCAGGTGGAGCAAGGTGAT 1185
QY 298 LeuValSerAlaTrpLysGluCysSerAspAspLeuLysGluCysLeuGlySerAlaVal 317
Db 1186 CTCCAGAAACGATGGAAACTGGTTCAGCAATAGACTCAAGGAATTTCCGAAATGTATCAT 1245
QY 318 IleProLeuCysSerIleAspLeuSerValGlyLeuCysArgHisArgAlaLeuLeuPheLysVal 337
Db 1246 CTTCTATAGGTAGTCTAACAAATGGGCTTTGCCGGCATCGTGCCATCTCTATTAAAGAA 1305
QY 338 LeuAlaAspSerIleAspLeuProCysArgIleAlaLysGlyCysLysTyrCysThrArg 357
Db 1306 TTGGCTGATTACATAGGTTTACCATTGTCGATAGCTCGAGGTTCAGATACTGTAAAGAG 1365
QY 358 AspAspAlaSerSerCysLeuValArgPheGly-----LeuAspArgGluTyr 373
Db 1366 AGCCACCAATCTTCTTCGCTTGTCAAGATTGACGATGACAGGAAGCTTTCAAGGGAATAT 1425
QY 374 LeuIleAspLeuIleGlyArgProGlyCysLeuCysGlnProAspSerLeuLeuAsnGly 393
Db 1426 GTAGTTGACCTCATCGGGGAACCAAGGAATGTCCATGATCCGGATTCCTCTATCAACGGT 1485
QY 394 ProSerSerIleSerIleSerSerProLeuArgPheProArgLeuLysProIleGluSer 413
Db 1486 GAAACACAGTGTACAGATTCTCTTACCTCTTCAAAATGAGTCATCTT----- 1530

QY 414 ThrIleAspPheArgSerLeuAlaLysGlnTyrPheLeuAspSerGlnSerLeuAsnLeu 433
Db 1530 ----- 1530
QY 434 ValPheAspGluAlaSerSerGlyAsnValValSerGlyLysAspAlaAlaPheSerVal 453
Db 1531 -----ACAGAT 1536
QY 454 TyrGlnArgProLeuAsnArgLysAspValAspGlyLysThrIleValValThrGlyAsp 473
Db 1537 TTTTCCAGGCCTTGCGTGCATAGTACATCTCTTGTGACACTGTA----- 1581
QY 474 LysAspArgAsnSerGlnLeuLeuAsnLysLysAlaAlaGlnLeuAsnThrGlnAspGly 493
Db 1582 GAGTCAAAGACTTCACGCACCTCTTCTGAAACACATTCAACGTTCAGGGAGTCAAGGCCAA 1641
QY 494 LysSerGluGlnPhe----- 498
Db 1642 GTACACAAAGAATTTGAGTTGCCTGATAACGCAGGGACAGTATGTTGTGCTCATATTGAT 1701
QY 499 ArgSerCysValAlaSerProTyrSerValGlnSerThrProPheValGluAsnValVal 518
Db 1702 CAAACTTGCTGTGCAAAAGTATCATCAATGGTTTTTGACAGAATCTGTTCTTCGAGCTCTA 1761
QY 519 ProLeuSerHisIleSerHisIleGlySerGluAsp-----Ser 531
Db 1762 CCACTTGAT---ATACCAAACCTTAGTGAAGAAAGATTGCCCCACAAGAAACCTGCAAA 1818
QY 532 GluHisLeuLeuAlaLeuSerHisPro----- 540
Db 1819 GAAGAAACCGTTCTATTAGAAGATCCAAACAGCTATGAAGCAGCCAAACTTATCAGTTGAA 1878
QY 541 -----ArgMetAspHisValAsnLeuProPheValHis 552
Db 1879 CCAGAGATAGTAGAGGCTGACACTCGAAAGATAAAAGGAAGGTTACCTGTTGACGCC 1938
QY 553 GlySerGlnLeuIleArgLysProAsnGluLeuSerLeuGlyLeuGluAspLeuValIle 572
Db 1939 ATCTCACCTTACTTG-----ACTATTGAACCTTCTTTGGCATCAGATTGGCTGGAGTTC 1992
QY 573 ProTrpThrAspLeuAspLeuArgGluLysIleGlyAlaGlySerPheGlyThrValTyr 592
Db 1993 TCATGGAATGAATTACATATCAAAGACCGTGTGGTGCTGGATCATTTTGGAACTGTTTCA 2052
QY 593 ArgGlyGluTrpHisGlySerAspValAlaValLysIleLeuThrGluGlnAspPheHis 612
Db 2053 CGTGCTGAGTGGCATGGATCAGATGTTGCTGTCAAGATTTTGTCTATTCAAGATTTCCAT 2112
QY 613 ProGluArgValAsnGluPheLeuArgGlu-----ValAlaIleMetLys 627
Db 2113 GATGACCAATTTCAGAGAAATTTCTCAGAGAGGTATGTAAAGCAACGGTTGCTATATAGAA 2172
QY 628 SerLeuArgHisProAsnIleValLeuPheMetGlyAlaValThrLysProProAsnLeu 647
Db 2173 CGTGTTCGTCAACCAAAATGTTGTTCTTCTCATGGGTGCTGTGACAGAGCGACCCCGGTA 2232
QY 648 SerIleValThrGluTyrLeuSerArgGlySerLeuTyrArgLeuLeuHisLysSerGly 667
Db 2233 TCAATAATAACAGATAATTTGCCAAGAGCAGTCTTTTTCGCCCTTATCCATAGGCCAGCT 2292
QY 668 VallysAsp---IleAspGluThrArgArgIleAsnMetAlaPheAspVal----- 683
Db 2293 TCTGGGAGTTGTAGATCAGAGGAGGAGGTACGTATGGCATTGGATGTGTTGTGCT 2352
QY 684 -----AlaLysGlyMetAsnTyrLeuHisArgArgAspProProIleValHis 699
Db 2353 ATTCCCCATTATGCCAAGGGGCTCAACTACCTACACTGTCTTAAATCCTCCTGTAGTGCAT 2412
QY 700 ArgAspLeuLysSerProAsnLeuLeuValAspLysLysTyrThrValLysValCysAsp 719
Db 2413 TGGGACCTGAAATCTCCAAATCTACTGTTGATAAGAACTGGACAGTGAAGGTTTTCGAT 2472

QY 720 PheGlyLeuSerArgLeuLysAlaArgThrPheLeuSerSerLysSerAlaAlaGlyThr 739
 Db 2473 TTTGGACTTTTCAAGATTCAAGCAACACATTTTCATACCAATCAAAATCTGTTCAGGAACA 2532
 QY 740 ProGluTrpMetAlaProGluValLeuArgAspGluProSerAsnGluLysSerAspVal 759
 Db 2533 CCTGAGTGGATGGCTCCAGAGTTTCTTAGAGGGGAACCGACAACGAGAAATCAGATGTT 2592
 QY 760 TyrSerPheGlyValIleLeuTrpGluLeuAlaThrLeuGlnGlnProTrpCysAsnLeu 779
 Db 2593 TACAGTTTCGGAGTAGTCTTATGGGAGTTGATTACTTTTGCACAGCCTTGGAAATGGACTC 2652
 QY 780 AsnProAlaGlnValAlaAlaValGlyPheLysGlyLysArgLeuAspIleProArg 799
 Db 2653 AGTCCTGCTCAGGTGGTGGAGCAGTTGCATTCAGAACAGGGCGCTTATAATTCCTCCC 2712
 QY 800 AspValAsnProLysLeuAlaSerIleValAlaCysTrpAlaAspGluProTrpLys 819
 Db 2713 AACACCTCTCCGGTTTGGTATCTCTAATGGAAGCTTGTGGCAGATGAGCCGTCCTCAG 2772
 QY 820 ArgProSerPheSerIleMetGluThrLeuLysProMetThrLysGlnAlaProPro 839
 Db 2773 CGGCCAGCATTTGGTAGTATAGTGGACACATTGAAGAGCCTACTAAAG---TCTCCGGTG 2829
 QY 840 Gln 840
 Db 2830 CAG 2832

RESULT 4

US-09-938-842A-1085
 ; Sequence 1085, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; TITLE OF INVENTION: SAME, AND METHODS OF USE
 ; FILE REFERENCE: SCRIP1300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 1085
 ; LENGTH: 2661
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-1085

Alignment Scores:

Pred. No.:	2,15e-117	Length:	2661
Score:	1193.00	Matches:	306
Percent Similarity:	48.12%	Conservative:	130
Best Local Similarity:	33.77%	Mismatches:	234
Query Match:	26.90%	Indels:	236
DB:	10	Gaps:	28

US-09-904-389-2 (1-850) x US-09-938-842A-1085 (1-2661)

QY 78 SerSerGlySerSerTyrAspAspSerSerLeuSerSerAspTyrTyrAla----- 94
 Db 133 ACTAGCCCTAGCCCTGCATCGACTTCTCCGCTCTCTCTCTCTGTTTGGTAACGCTTCC 192
 QY 95 -----ProThrLeuSer-----AsnProAlaAlaAsnGluIleAsnAlaLeuGlu 109
 Db 193 ACACAAATGCCGAGACTGGATACATTGAGCCCTGTTGGCCGCTGATCTGACGCGCTGTTGAT 252

QY 110 TyrIleLeuAspAspAspPheArgValMetLysAlaValGlySerGlyGlySerSerGly 129
 Db 253 GGTGTT-----GATTTCAATTTGATG----- 273
 QY 130 LysSerTrpAlaGlnGlnThrGluSerPheGlnLeuGlnGlnProLeuValLeuArg 149
 Db 274 -----GAGGAGGAGTACCAAGTCCAGTTAGCTATGGCGATCAGC 312
 QY 150 LeuSerSerAsp**ThrCysAlaAspAspProAsnPhenMetAspProIleProAspGlu 169
 Db 313 GTCTCT-----GATCTGATCCGAGAGAG 336
 QY 170 -----AlaAlaLeuArg---SerLeuSerIleSerAla--- 179
 Db 337 AATGCAGATACAGCTCAGCTTGATGCCGCTAAGAGGATTAGCCTTGGGTTTCTGCTCCG 396
 QY 180 -----GluAlaIleSerHisArgPheTrpValAsnGlyCys 191
 Db 397 GTCACCGACGCTGATTCGCCCGCTTGACTTCTCTCGCTTCGTTATTGG---TCGCTTGC 453
 QY 191 ----- 191
 Db 454 TCGATTAGCGAGGGTTTAAAGGAATTAGGATCTTGGCTATTGCCCTGCAGTGTCTCTTCG 513
 QY 192 -----MetSerTyrLeuGluLysVal 198
 Db 514 TTGCGAGTATTTCTGAATCCTAATTGTGGACATAAGGTCAATTAATTATGACCAGAAAGTC 573
 QY 199 ProAspGlyPheTyrLeuIleHisGlyMetAspProTyrValTrpSerLeuCysThrAsn 218
 Db 574 AGGGATGGATTTTACGATGTGTATGGG-----ATTACATCTAAT 612
 QY 219 LeuGlnGluAspGlyArgIleProSerPheGluSerLeuLysThrValAspSerIle 238
 Db 613 TCTCTTTTACAGGGGAGATGCCACTTCTTGTGATCTTCAAGCGATCTCTATTTCAGAT 672
 QY 239 GlySerSerIleGluValValLeuIleAspArgHisSerAspAlaSerLeuLysGluLeu 258
 Db 673 AATGTTGATTATGAGGTCAATCTAGTTAACAGATTGATTGATTCCTGAACACTACAAGAGCTA 732
 QY 259 GlnAsnArgValHisAsnIleSerSerSerCys-----ValThrThr 272
 Db 733 GAGAGGAGAGTATTCGCTTTGGCTTCGGAATGTCCAGACTTTGCTCCTGGTCCAGGTGTCA 792
 QY 273 LysGluValAlaAspHisIleAlaLysLeuValCysAsnHisLeuGlyGlySerValSer 292
 Db 793 AGTGATTGACTCAGAAAATTCGAAATATAGTTGTAGAGCAAAATGGTGGCCCGCTT--- 849
 QY 293 GluGlyGluAspAspLeuValSerAlaTrpLysGluCysSerAspAspLeuLysGluCys 312
 Db 850 GAAAATGCTGATGAAGCATTGAGAAGGTGGATGCTTCGGAGCTATGAACATAAGAAATCT 909
 QY 313 LeuGlySerAlaValIleProLeuCysSerLeuSerValGlyLeuCysArgHisArgAla 332
 Db 910 TTGAACACTACTATTCTTCCACTTGGTCCAGTTAATGTTGGTCTTGCACGACACAGGGCT 969
 QY 333 LeuLeuPheLysValLeuAlaAspSerIleAspLeuProCysArgIleAlaLysGlyCys 352
 Db 970 TTGCTTTTCAAGGCTCTTGTGCTGATAGGATTAATCTCCCATGATGCTGGTAAAGGCAGT 1029
 QY 353 LysTyrCysThrArgAspAspAlaSerSerCysLeuValArg----- 366
 Db 1030 TACTACACTGGAACCTGATGATGGGCTGTGAACCTTGATTAAACTAGATGACAAAAGTCCT 1089
 QY 367 -----PheGlyLeuAspArgGluTyrLeuIleAspLeuIleGlyArgProGlyCysLeu 384
 Db 1090 AATTCGTTCTTACATGTCAGTGAATACATATTATTGATTAAATGGGTGCTCCGGGTGCTCTG 1149
 QY 385 CysGln-----ProAspSerLeuLeu----- 391
 Db 1150 ATCCCTTCTGAGGTTTCAAGCAGTTTTTCTCCAGTTTCTTGCACAGATACAGAGATATTT 1209
 QY 392 ---AsnGlyProSerSerIleSerIleSerSerProLeuArgPheProArgLeuLys--- 409

Db 1210 CCTGAGAAATTTGGACTCTTTGCAACATTCATCCCGCTACTTGTGAGAAAGAAATGAAACG 1269
QY 410 -----ProileGluSerThrIleAspPheArgSer---LeuAlaLysGlnTyrPhe 425
Db 1270 CCAGCATTTTCAGTTTCGAAGGAGCAGATTCTAGATCTGGTATGGTAGCAAACTTCTTC 1329
QY 426 LeuAspSerGlnSerLeuAsn----- 432
Db 1330 ACTGGAACACAGGAAGAAACACATGACAGATGTCTGTGTGAAACACATCAACACAGAGAGA 1389
QY 433 -----LeuValPheAspGluAlaSerSerGlyAsnValVal--- 444
Db 1390 TTTGAGCATGATTTTGGGAAGTTAATGCACCTCACAGCAGATATCTGGTGAAATATGCCA 1449
QY 445 -----SerGlyLysAspAla----- 449
Db 1450 CCATTTTCTGGGAACCGACCTTGTGCACAGAAAGTTAAAGTTAAATGCTCAAGTAT 1509
QY 450 AlaPheSerValTyrGlnArgPro----- 457
Db 1510 GTCATAAGTGCAGCAAGAAACCCCTGAATTTGGCAGAAATTACATGCTGTGTGTAGAA 1569
QY 458 -----LeuAsnArgLysAspValAspGly 465
Db 1570 AGTGGTGATCACCTCCCCAGATTGTTTATGGATATTAACCCACATAACTTGAGGGGG 1629
QY 466 LysThrIleValValThrGlyAspLysAspArgAsnSerGlnLeuAsn----- 482
Db 1630 AAGAATTTGCTTCAAGAGCTCCGCCAAGAAAGTAGCAATCTATGGTTCTGCTATTCCA 1689
QY 483 -----LysLysAlaAlaGlnLeu-----AsnThrGlnAspGlyLysSerGlu 496
Db 1690 TGCTACCCAGAAAGGTAGCTGAACAACTGAGAGAAATCTGAAAGGAAACCCACAGCCGAG 1749
QY 497 GlnPheArgSerCysValAlaSerProTyrSerValGlnSerThrProPheValGluAsn 516
Db 1750 AGTTACCAACAATCAGTCGAGGTCGATTTGTCAATGAAGAGCAACTTTGATTGGATAAT 1809
QY 517 Val-----ValProLeuSerHisIleSerHisIleGlySerGluAspSerGluHisLeu 534
Db 1810 ACTGGTAAAGCTTTCTTCATCCGAAATATGGAGGTGGCACTGCTGATGGGAGTCTGCT 1869
QY 535 LeuAlaLeuSerHisProArgMetAspHisValAsnAsnLeuProPheValHisGlySer 554
Db 1870 GTTTGTGATAGTCATGACCAA----- 1890
QY 555 GlnLeuIleArgLysProAsnGluLeuSerLeuGlyLeuGluAspLeuVal----- 571
Db 1891 -----GGGATTAATCCATTCCTCGGAGAGCT 1917
QY 572 -----IleProTrpThrAspLeuAspLeuArgGluLysIleGlyAlaGlySer 587
Db 1918 GCAAAGTGGGAATATATGTGGGAAGATCTTCAGATTGGCAGCGCATTTGTTGTTCA 1977
QY 588 PheGlyThrValTyrArgGlyGluTrpHisGlySerAspValAlaValLysIleLeuThr 607
Db 1978 TATGGAGAAGTTTATCGTCGAGAGTGGAAATGGAATGAACTGAAGTGGCTGTTAAGAAGTTTCTG 2037
QY 608 GluGlnAspPheHisProGluArgValAsnGluPheLeuArgGluValAlaIleMetLys 627
Db 2038 GACCAAGATTTCTCTGGTGATGCATTCACACAGCTCAAATCTGAAATGAAATAATGTTG 2097
QY 628 SerLeuArgHisProAsnIleValLeuPheMetGlyAlaValThrLysProAsnLeu 647
Db 2098 AGGTTACGGCATCCAAACGTTGTTCTTTTCATCGGAGCAGTTACTCGTCCCCCAATTTC 2157
QY 648 SerIleValThrGluTyrLeuSerArgGlySerLeuTyrArgLeuLeuHisLysSerGly 667
Db 2158 TCCATCTGACAGAGTTCTTACCCAGGGGAAGTTGTATAGATTACTCCATCGGCCGAAC 2217
QY 668 ValLysAspIleAspGluThrArgArgIleAsnMetAlaPheAspValAlaLysGlyMet 687

Db 2218 ---CATCAGCTTGATGAGAGAGGAGAAATGCGGATGGCTCTTGATGTGGCAAGGAATG 2274
QY 688 AsnTyrLeuHisArgAspProProIleValHisArgAspLeuLysSerProAsnLeu 707
Db 2275 AACTACTTACACACACAGCCACCGACTGTTGTACATAGGGATTTAAATCTCCAAACCTT 2334
QY 708 LeuValAspLysLysTyrThrValLysValCysAspPheGlyLeuSerArgLeuLysAla 727
Db 2335 CTGTGTTGATAAAATTTGGTTGTGAAGGTTTGTGATTTGGATTGTCCCGCATGAAACAC 2394
QY 728 ArgThrPheLeuSerSerLysSerAlaAlaGlyThrProGluTrpMetAlaProGluVal 747
Db 2395 CACACATATTTGTCCTCGAAATCAACTGCAGGAACGCTGAGTGGATGGCTCCGAAAGTG 2454
QY 748 LeuArgAspGluProSerAsnGluLysSerAspValTyrSerPheGlyValIleLeuTrp 767
Db 2455 TTGAGGAATGAACCGGCTAATGAGAAATGTGACGTGTACAGCTTTGGTGTCAATTTGG 2514
QY 768 GluLeuAlaThrLeuGlnGlnProTrpCysAsnLeuAsnProAlaGlnValValAlaAla 787
Db 2515 GAATTAGCTACTTCACGCTCCCTCGAAAGGTTTGAACCGATGCAAGTCGTTGGAGCT 2574
QY 788 ValGlyPheLysGlyLysArgLeuAspIleProArgAspValAsnProLysLeuAlaSer 807
Db 2575 GTGGGATTCAGAAATCGACGCTTGAATCCAGATGATATCGATCTAACTGTGGCAGAG 2634
QY 808 LeuIleValAlaCysTrp 813
Db 2635 ATAATCCGTGAATCTTGG 2652
RESULT 5
US-09-938-842A-1577
; Sequence 1577, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1577
; LENGTH: 2211
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1577
Alignment Scores:
Pred. No.: 5.83e-76 Length: 2211
Score: 806.00 Matches: 170
Percent Similarity: 59.75% Conservative: 72
Best Local Similarity: 41.98% Mismatches: 135
Query Match: 18.17% Indels: 28
DB: 10 Gaps: 7
US-09-904-389-2 (1-850) x US-09-938-842A-1577 (1-2211)
QY 457 ProLeuAsnArgLysAspValAspGlyLysThrIleValValThrGlyAspLysAspArg 476
Db 973 CCTATCTTAAGAAACGGTATCAAT--AAGTCAGCATGTGGCAGTGGAGGTAGTCTTAAG 1029
QY 477 AsnSerGlnLeuLeuAsnLysLysAlaAlaGlnLeuAsnThrGlnAspGlyLysSerGlu 496


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Db 1030 GCTTCTAATGAGTACCTGCACGGCTTTTCAGAGCAAT---GGCAATGGAACCAAAA 1086
Qy 497 GlnPheArgSerCysValAlaSerProTyrSerValGlnSerThrProPheValGluAsn 516
Db 1087 AGGCTGAAGTGAATTTTCAGATGTCTATGGAATGGAGCTGAGGGTTTCATACATAAT 1146
Qy 517 ValValProLeuSerHisIleSerHisIleGlySerGlu-----Asp 530
Db 1147 GGAGATCGCTTTCAGTATATTGGGAACCTGGGACAAAGTAACCTCCACAGGACTAGAG 1206
Qy 531 SerGluHisLeuLeuAlaLeuSerHisProArgMetAspHisValAsnAsn----- 547
Db 1207 AGTGGTTTGGTGTCTGTCATGCGGGGAACAAATAATGCGGACCTAAATGCTGAGATAGAA 1266
Qy 548 -----LeuProPheVal-----HisGly 553
Db 1267 GATGCTTGGAACTACCTGCTTGTAGTGTGATCCCTTGCAATTTAGGAGTCAACAGCGGT 1326
Qy 554 SerGlnLeu-----IleArgLysProAsnGluLeuSerLeuGlyLeuGluAspLeuVal 571
Db 1327 AGGCAACAAAGTCTGTCAACCAAGGAATAATAGATTAGTTACTGATTCGTATGTGAG 1386
Qy 572 IleProTrpThrAspLeuAspLeuArgGluLysIleGlyAlaGlySerPheGlyThrVal 591
Db 1387 ATACGATGGGAAGATCTACAACCTGGGAGGAGGTGCGAAGAGGTTTCATTTGTCGGGT 1446
Qy 592 TyrArgGlyGluTrpHisGlySerAspValAlaValLysIleLeuThrGluGlnAspPhe 611
Db 1447 CATCGTGGAGTTTGAATGGATCGGATGTTGCTATTAAAGTTTACTTCGATGTTGATTAC 1506
Qy 612 HisProGluArgValAsnGluPheLeuArgGluValAlaIleMetLysSerLeuArgHis 631
Db 1507 AATGCGATGACTTTGACGGAGTGCAGAAAGGAGATCAACATTATGAAGAACTGAGACAT 1566
Qy 632 ProAsnIleValLeuPheMetGlyAlaValThrLysProProAsnLeuSerIleValThr 651
Db 1567 CCGAATGTGCTACTATTATGGGAGCAGTATGTACAGAAGAAATACTGCCATATCATG 1626
Qy 652 GluTyrLeuSerArgGlySerLeuTyrArgLeuLeuHisLysSerGlyValLysAspIle 671
Db 1627 GAATATATGCCAAGAGGGAGTCTCTCAAAATACTTCAATAATACGAAT---CAGCCATTG 1683
Qy 672 AspGluThrArgArgIleAsnMetAlaPheAspValAlaLysGlyMetAsnTyrLeuHis 691
Db 1684 GACAAGAAACGCCCTTTAAGAAATGGCCCTTGATGTTGCTAGGGGAATGAATTAATACT 1743
Qy 692 ArgArgAspProIleValHisArgAspLeuLysSerProAsnLeuLeuValAspLys 711
Db 1744 CGCAGAAATCCGCCAATTTACATAGAGACTTGAATCTTCCAATCTACTCGTGACAAG 1803
Qy 712 LysTyrThrValLysValCysAspPheGlyLeuSerArgLeuLysAlaArgThrPheLeu 731
Db 1804 AACTGGAATGTCAAGTTGGAGACTTTGGGTTATCAAGTGGGAAGAACCGAACCTTCTTG 1863
Qy 732 SerSerLysSerAlaAlaGlyThrProGluTrpMetAlaProGluValLeuArgAspGlu 751
Db 1864 AGTACTAAATCCGGGAAAGGAACCTCCGAGTGGATGGCTCCTGAAGTTCTCAGAAAGTGA 1923
Qy 752 ProSerAsnGluLysSerAspValTyrSerPheGlyValIleLeuTrpGluLeuAlaThr 771
Db 1924 CCTTCGAATGAGAAGTGTGATGTGTTCAGCTTTGGAGTCACTTATGGGAGCTAATGACT 1983
Qy 772 LeuGlnGlnProTrpCysAsnLeuAsnProAlaGlnValValAlaValGlyPheLys 791
Db 1984 ACCTTAGTACCATGGGACCGTTTGAACCTCTATTCAAGTTGTTGGAGTTGTTGTTTCATG 2043
Qy 792 GlyLysArgLeuAspIleProArgAspValAsnProLysLeuAlaSerLeuIleValAla 811
Db 2044 GATCGACGATTAGACTTACCTGAAGGATTAAATCCCGGATCGCATCCATATACAGGAT 2103
Qy 812 CysTrpAlaAspGluProTrpLysArgProSerPheSerIleMetGluThrLeuLys.831
Db 2104 TGTGGCAAACTGATCCAGCAAAACGACCGTTCGTCGAGGAATTAATTACTCAGATGATG 2163
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Qy 832 ProMetThrLysGln 836
Db 2164 AGCCTGTTCGCAAA 2178
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RESULT 6

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US-09-938-842A-1014
; Sequence 1014, Application US/09938842A
; Patent No. US20020160378A1
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```
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
```

```
; APPLICANT: Kreps, Joel
```

```
; APPLICANT: Wang, Xun
```

```
; APPLICANT: Zhu, Tong
```

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; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
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; CURRENT APPLICATION NUMBER: US/09/938,842A
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; PRIOR FILING DATE: 2001-08-24
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; PRIOR APPLICATION NUMBER: US 60/227,866
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; PRIOR FILING DATE: 2000-08-24
```

```
; PRIOR APPLICATION NUMBER: US 60/264,647
```

```
; PRIOR FILING DATE: 2001-01-16
```

```
; PRIOR APPLICATION NUMBER: US 60/300,111
```

```
; PRIOR FILING DATE: 2001-06-22
```

```
; NUMBER OF SEQ ID NOS: 5379
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; SEQ ID NO 1014
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; LENGTH: 1662
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; TYPE: DNA
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; ORGANISM: Arabidopsis thaliana
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US-09-938-842A-1014
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Alignment Scores:

Pred. No.:	9.59e-53	Length:	1662
Score:	588.00	Matches:	165
Percent Similarity:	51.06%	Conservative:	99
Best local Similarity:	31.91%	Mismatches:	174
Query Match:	13.26%	Indels:	81
DB:	10	Gaps:	21

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US-09-904-389-2 (1-850) x US-09-938-842A-1014 (1-1662)
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Qy 346 CysArgIleAlaLysGlyCysLysTyrCysThrArgAspAspAlaSerSerCysLeuVal 365
Db 201 TGCTCGATATGCTTTGGATGATAA---TGTTG-AGAGAGCAGAGATGTACTACTCATC 256
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```
Qy 366 ArgPheGlyLeuAsp-----ArgGluTyrLeuIleAspLeuIleGlyArg 380
Db 257 AGA-----GATGTTGAAATTTGGCTGAAGATCCTGCTACTAGACCTGTTTCGAAG 307
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Qy 381 ProGlyCysLeuCysGlnProAspSerLeuLeuAsnGly-----Pro 394
Db 308 TT-CGTTGTGTG---CAGGTTTCTCCACATTTGAATGGAAATTTCTGGTGACGTGATCCT 363
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Qy 395 SerSerIleSerIleSerProLeuArgPheProArgLeuLysProIleGluSerThr 414
Db 364 TCGGATCCTGCGGTCAAT-----GAAGATGCTCAAGCTCC 399
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Qy 415 IleAspPheArgSerLeuAlaLysGlnTyrPheLeuAspSer-----GlnSerLeu 431
Db 400 TATAACTCGAGGTCTCTTGACCTCCCACTTTTGGTCTTCTCCGAAATTTTCGAAGCTCTT 459
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```
Qy 432 AsnLeuValPhe-----AspGluAlaSerSerGlyAsnValVal 444
Db 460 ACTCAAGCTTACAAGATCATGCTCAAGACGATGATAGTGTCTCAATGCACAGTGCCT 519
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Qy 445 SerGlyLys-----AspAlaAlaPheSerValTyrGlnArgProLeuAsnArgLys 461
Db 520 AATTCTCGACCGATGACGAAATCACCTTTTCTACAATGCACAGGCGG-----567
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Qy 462 AspValAspGlyLysThrIleValValThrGlyAspLysAspArgAsnSerGlnLeuLeu 481
Db 568 AAATCCTTAGTCAGCTAACTTCCATGCTTGGTGAACCTTGATTAATATTTCAA-----621
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QY 482 AsnLysLysAlaAlaGlnLeuAsnThrGlnAspGlyLysSer---GluGlnPheArgSer 500
Db 622 -----GAGGCTCATGCTTTCTTCTACCGCGATGGTTCTCTCTCGATGATATT----- 669
QY 501 CysValAlaSerProTyrSerValGlnSerThrProPheValGluAsnValProLeu 520
Db 670 ---GTTGTGTGATGGTGGTCGAGGAGGATCAACCTGTTCAAAACAG----- 714
QY 521 SerHisIleSerHisIleGlySerGluAspSerGluHisLeuLeuAlaLeuSerHisPro 540
Db 715 AAATCTATCACTTTCTTTGAGCATGACAAATCAACCAACGAGCTG----- 759
QY 541 ArgMetAspHisValAsnAsnLeuProPheValHisGlySerGlnLeuLeuArgLysPro 560
Db 760 -----CTACCT-----CGTGTGTGTGAATACCT 783
QY 561 AsnGluLeuSerLeuGlyLeuGluAspLeuValIleProTyrThrAspLeuAspLeuArg 580
Db 784 ACGGAT-----GGAACGTGATGAGTGGGAAATTGACATGAAGCAGCTCAAAATTGAA 834
QY 581 GluLysIleGlyAlaGlySerPheGlyThrValTyrArgGlyGluTyrHisGlySerAsp 600
Db 835 AAAAAGGTGGCATGTGATCATACCGGGAACCTATTTAGAGAAACCTATTGTAGTCAGGAA 894
QY 601 ValAlaValLysIleLeuThrGluGlnAspPheHisProGluArgValAsnGluPheLeu 620
Db 895 GTAGCTATCAAAATCTCAAGCCTGAGCGTGTAAATGCGGAAATGCTACGAGAGTTTCT 954
QY 621 ArgGluValAlaIleMetLysSerLeuArgHisProAsnIleValLeuPheMetGlyAla 640
Db 955 CAGGAAGTATATATATATAGGAAAGTTCCGCATAAAATGTTCCAGTTTCATTGGTGCA 1014
QY 641 ValThrLysProProAsnLeuSerIleValThrGluTyrLeuSerArgGlySerLeuTyr 660
Db 1015 TGTACAGCATCACCAAAACCTCTGCATTGTGACAGAGTTTCATGACTCGGGGAGCAATTAT 1074
QY 661 ArgLeuLeuHisLys---SerGlyValLysAspIleAspGluThrArgArgIleAsnMet 679
Db 1075 GATTTCCTTCACAAACACAAAGGGGTTTTTAAATTCATCTTTG-----CTCAAAGTG 1128
QY 680 AlaPheAspValAlaLysGlyMetAsnTyrLeuHisArgArgAspProProIleValHis 699
Db 1129 GCACCTGACGTCTCGAAGGAATGAATTATCTGCATCAAAACAAT-----ATTATTCTAT 1182
QY 700 ArgAspLeuLysSerProAsnLeuLeuValAspLysLysTyrThrValLysValCysAsp 719
Db 1183 AGAGACCTTAAGACTGTCTAATCTCTTCTTATGGACCAACATGAAGTTGTCAAAGTTGCCGAT 1242
QY 720 PheGlyLeuSerArgLeuLysAlaArgThrPheLeuSerSerLysSerAlaAlaGlyThr 739
Db 1243 TTTGGTGTGCCAGAGTGCAGACTGAGTCAGGGGTTATGACA---CGGAAACAGGGGACA 1299
QY 740 ProGluTrpMetAlaProGluValLeuArgAspGluProSerAsnGluLysSerAspVal 759
Db 1300 TACCGATGGATGGCTCCAGAGTCAATTGAGCACAAACCTTATGATCACAGGGCAGATGTC 1359
QY 760 TyrSerPheGlyValIleLeuTrpGluLeuAlaThrLeuGlnGlnProTyrCysAsnLeu 779
Db 1360 TTCAGCTACCGGATTTGCTGTGGGAACTTTTGACTGGGGAACTCCCATATCTTACTTTG 1419
QY 780 AsnProAlaGlnValAlaAlaValGlyPheLysGlyLysArgLeuAspIleProArg 799
Db 1420 ACTCCACTGCAAGCTGCTGTTGGCGTTGTCCAAAAGGAGCTTAGACCCAAAATTCCAAAG 1479
QY 800 AspValAsnProLysLeuAlaSerLeuIleValAlaCysTrpAlaAspGluProTyrLys 819
Db 1480 GAAACACACCCCAAAACTGACTGAATCTTGTAGAAATGCTGGCAGCAGCAAGACCCAGCTCTA 1539
QY 820 ArgProSerPheSerIleMetGluThrLeuLysProMetThrLysGln 836
Db 1540 AGACCAATTTTGCAGAAATCATAGAAATGCTTAACCAACTAATCCCGGAG 1590

RESULT 7
US-09-938-842A-903
; Sequence 903, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 903
; LENGTH: 1638
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-903

Alignment Scores:
Pred. No.: 1.06e-44 Length: 1638
Score: 513.00 Matches: 157
Percent Similarity: 43.74% Conservative: 84
Best Local Similarity: 28.49% Mismatches: 149
Query Match: 11.57% Indels: 163
DB: 10 Gaps: 18

US-09-904-389-2 (1-850) x US-09-938-842A-903 (1-1638)
QY 345 ProCysArgIleAlaLysGlyCysLys----- 353
Db 201 CCCTGCCAGGTATGCTTTGGATGTGAATGTGGAGAGGGCTGAAGACGCTTGTGATGCACAA 260
QY 354 -----TyrCysThrArgAspAspAlaSerSerCysLeuValArgPhe----- 367
Db 261 GCGATTGCTGCATTCTGCTTACGATCCCCAGAAATCGGCCTGCTATCG--AAGTTTCATCTCG 319
QY 368 -----Gly 368
Db 320 TCCAGCCTGATCTTTTCATCTTTTATGTTTGCCTCTTTTGTCAACTTTTGGATTCTCTGGG 379
QY 369 LeuAspArgGluTyrLeuIleAspLeuIleGlyArg-----ProGlyCysLeuCys 385
Db 380 CTCACAGGTTCTTTTCGTCACCTCTCTTTTCTTAAGGTTCAACCTGCCGGGATCTCTGCTG 439
QY 386 GlnProAspSerLeuLeuAsn-----GlyProSerSerIleSerIleSer 400
Db 440 ACTTG-GACTCTACTTCTTAATGATGCTGGTCACTTCTCTCTACCCGAAAAGCATTCAT 498
QY 401 SerProLeuArgPheProArgLeuLysProIleGluSerThrIleAspPheArgSerLeu 420
Db 499 CCGCCGCTGCTCTTTGGTTTCATCCCTAATCTTGAAGCAGCTTGCATTTGCAGCTAGTTTA 558
QY 421 AlaLysGlnTyrPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAlaSerSer 440
Db 559 TCCCAA-----GACGAGGATGCAGAC 579
QY 441 GlyAsnValValSerGlyLysAspAlaPheSerValTyrGlnArgProLeuAsnArg 460
Db 580 AACTCTGTTTCAACAAT-----TCACTCTATTACCGGCCCTTGCAT--- 621
QY 461 LysAspValAspGlyLysThrIleValValThrGlyAspLysAspArgAsnSerGlnLeu 480
Db 622 -----GAGATAACCTTTTCCACAGACAGCAAGCCTAAACTCCTTTTTCAG 666

QY 724 gLeuLysAlaArgThrPheLeuSerSerLysSerAlaAlaGlyThrProGluTrpMetAl 744
Db 426 GTTCCATAACCATACA-----ACACATGTCCTGGTTGGAACTTTCCCATGGATGGC 373
QY 744 aProGluValLeuArgAspGluProSerAsnGluLysSerAspValTrpSerPheGlyVa 764
Db 372 TCCAGAGTTATCCAGAGTCTCCCTGTGTGAGAACTTGTGACACATATTCCTATGGTGT 313
QY 764 lLeuLeuTrpGluLeuAlaThrLeuGlnGlnProTrpCysAsnLeuAsnProAlaGlnVa 784
Db 312 GGTTCCTCTGGGAGATGCTAACAAAGGAGGTCCCTTTAAAGGTTTGGAAAGGATTACAAGT 253
QY 784 lValAlaAlaValGlyPheLysGlyLysArgLeuAspIleProArgAspValAsnProLy 804
Db 252 AGCTTGGCTTGTAGTGGAAAAAAGAGAGATTAAACCATTCGAAGCAGTTGCCCCAGAAG 193
QY 804 sLeuAlaSerLeuIleValAlaCysTrpAlaAspGluProTrpLysArgProSerPheSe 824
Db 192 TTTTGTGAACTGTTACATCAGTGTGGGAAGCTGATGCCAAGAAACGGCCATCATTTCAA 133
QY 824 rSerIleMetGluThrLeuLysProMetThr 834
Db 132 GCAATCATTTCAATCCTGGAGTCCATGTCA 102

RESULT 9
US-09-757-982-6
; Sequence 6, Application US/09757982
; Patent No. US20020094559A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/757,982
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 09/163,115
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
US-09-757-982-6

Alignment Scores:
Pred. No.: 6.53e-44 Length: 1365
Score: 504.50 Matches: 112
Percent Similarity: 55.84% Conservative: 41
Best Local Similarity: 40.88% Mismatches: 106
Query Match: 11.38% Indels: 15
DB: 9 Gaps: 4

US-09-904-389-2 (1-850) x US-09-757-982-6 (1-1365)
QY 564 SerLeuGlyLeuGluAspLeuValIleProTrpThrAspLeuAspLeuArgGluLysIle 583
Db 7 TCTCTCGGTGCCTCCTTTGTGCAAAATTAAATTTGATGACTTGCAGTTTGTGAAACTGC 66
QY 584 GlyAlaGlySerPheGlyThrValTrpArgGlyGluTrpHisGlySerAsp-----Val 601
Db 67 GGTGGAGGAAGTTTGGGAGTGTATTATCGAGCCCAATGGATATCACAGGACAAGGAGGTG 126
QY 602 AlaValLysIleLeuThrGluGlnAspPheHisProGluArgValAsnGluPheLeuArg 621
Db 127 GCTGTAAAGAAGCTCCTCAAATAGAG-----AAA 156
QY 622 GluValAlaIleMetLysSerLeuArgHisProAsnIleValLeuPheMetGlyAlaVal 641
Db 157 GAGGCAGAAATACTCAGTGTCTCAGTCACAGAAACATCATCCAGTTTATGGAGTAATT 216

QY 642 ThrLysProProAsnLeuSerIleValThrGluTrpLeuSerArgGlySerLeuTrpArg 661
Db 217 CTTGAACCTCCCAACTATGGCATTGTACAGAAATATGCTTCTCTGGGATCACTCTATGAT 276
QY 662 LeuLeuHisLysSerGlyValLysAspIleAspGluThrArgArgIleAsnMetAlaPhe 681
Db 277 TACATTACAGTAACAGAAAGTACAGAGATGGATATGGATCACATTATGACCTGGGCCACT 336
QY 682 AspValAlaLysGlyMetAsnTrpLeuHisArgArgAspPro---ProIleValHisArg 700
Db 337 GATGTAGCCCAAGGAATGCATTATTACATATGAGGCTCTGTCAAGGTGATTACAGA 396
QY 701 AspLeuLysSerProAsnLeuValAspLysLysTrpThrValLysValCysAspPhe 720
Db 397 GACCTCAAGTCAAGAAACGTTGTTATAGCTGCTGATGGAGTACTGAAGATCTGTGACTTT 456
QY 721 GlyLeuSerArgLeuLysAlaArgThrPheLeuSerSerLysSerAlaAlaGlyThrPro 740
Db 457 GGTGCTCTCGGTTCCATAACCATACA-----ACACACATGTCCTTGGTTGGAACTTTC 510
QY 741 GluTrpMetAlaProGluValLeuArgAspGluProSerAsnGluLysSerAspValTrp 760
Db 511 CCATGGATGGTCCAGAGTTATCCAGAGTCTCCCTGTGTGAGAACTTGTGACACATAT 570
QY 761 SerPheGlyValIleLeuTrpGluLeuAlaThrLeuGlnGlnProTrpCysAsnLeuAsn 780
Db 571 TCCTATGGTGTGCTCTCTGGGAGATGCTAAACAAGGGAGGTCCTTTAAAGGTTTGGAA 630
QY 781 ProAlaGlnValValAlaAlaValGlyPheLysGlyLysArgLeuAspIleProArgAsp 800
Db 631 GGATTACAAGTAGCTGGCTTGTAGTGGAAAAAACAAGAGAGATTAAACCATTCGAAGCAGT 690
QY 801 ValAsnProLysLeuAlaSerLeuIleValAlaCysTrpAlaAspGluProTrpLysArg 820
Db 691 TGCCCCAGAAGTTTGTGTAACACTGTTTACATCAGTGTGGGAAGTGTATGCCAAGAAACGG 750
QY 821 ProSerPheSerSerIleMetGluThrLeuLysProMetThr 834
Db 751 CCATCATTTCAAGCAAAATCATTTCAATCCTGGAGTCCATGTCA 792

RESULT 10
US-09-757-982-4
; Sequence 4, Application US/09757982
; Patent No. US20020094559A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/757,982
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 09/163,115
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2120
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (47)..(1411)
US-09-757-982-4

Alignment Scores:
Pred. No.: 1.3e-43 Length: 2120
Score: 504.50 Matches: 112
Percent Similarity: 55.84% Conservative: 41
Best Local Similarity: 40.88% Mismatches: 106
Query Match: 11.38% Indels: 15
DB: 9 Gaps: 4

US-09-904-389-2 (1-850) x US-09-757-982-4 (1-2120)

QY 564 SerLeuGlyLeuGluAspLeuValIleProTrpThrAspLeuAspLeuArgGluLysIle 583
Db 53 TCCTCGTGGTCCCTCTTTGTGCAATTAATTTGATGACTTGCAGTTTGTGAAACTGC 112
QY 584 GlyAlaGlySerPheGlyThrValTyrArgGlyGluTrpHisGlySerAsp-----Val 601
Db 113 GGTGAGGAAGTTTGGGAGTGTTCATCGACCAATGGATATCACAGGACAGGAGGTG 172
QY 602 AlaValLysIleLeuThrGluGlnAspPheHisProGluArgValAsnGluPheLeuArg 621
Db 173 GGTGTAAGAAGCTCCTCAAAATAGAG-----AAA 202
QY 622 GluValAlaIleMetLysSerLeuArgHisProAsnIleValLeuPheMetGlyAlaVal 641
Db 203 GAGGAGAAATACTCAGTGTCTCAGTCACAGAAACATCATCCAGTTTATGAGTAAT 262
QY 642 ThrLysProProAsnLeuSerIleValThrGluTyrLeuSerArgGlySerLeuTyrArg 661
Db 263 CTTGAACCTCCCAACTATGGCATTTGTCAGAAATATGCTTCTCTGGGATCACTCTATGAT 322
QY 662 LeuLeuHisLysSerGlyValLysAspIleAspGluThrArgArgIleAsnMetAlaPhe 681
Db 323 TACATTAACAGTAACAGAAAGTGAGGAGATGGATATGGATCACATTATGACCTGGGCACT 382
QY 682 AspValAlaLysGlyMetAsnTyrLeuHisArgArgAspPro---ProIleValHisArg 700
Db 383 GATGTAGCCAAAGGAATGCATTATTACATATGATGGAGCTCCTCAAGGTGATTCACAGA 442
QY 701 AspLeuLysSerProAsnLeuValAspLysLysTyrThrValLysValCysAspPhe 720
Db 443 GACCTCAAGTCAAGAAACGTTGTTATAGTGTCTGATGGAGTACTGAAGATCTGTGACTTT 502
QY 721 GlyLeuSerArgLeuLysAlaArgThrPheLeuSerSerLysSerAlaAlaGlyThrPro 740
Db 503 GGTGCTCTCGTTCATCAACCATACA-----ACACACATGTCCTTGGTGGAACTTTC 556
QY 741 GluTrpMetAlaProGluValLeuArgAspGluProSerAsnGluLysSerAspValTyr 760
Db 557 CCATGGATGGCTCCGAAGTTATCCAGAGTCTCCCTGTGTGAGAAACTTGTGACACATAT 616
QY 761 SerPheGlyValIleLeuTrpGluLeuAlaThrLeuGlnGlnProTrpCysAsnLeuAsn 780
Db 617 TCCTATGGTGTGGTCTCTGGGAGATGCTAAACAGGAGGAGTCCCTTTAAAGGTTTGAA 676
QY 781 ProAlaGlnValValAlaAlaValGlyPheLysGlyLysArgLeuAspIleProArgAsp 800
Db 677 GGATTACAAGTAGCTGGCTTGTAGTGGAAGAAACAGAGAGATTAAACCATTCACAGCAGT 736
QY 801 ValAsnProLysLeuAlaSerLeuIleValAlaCysTrpAlaAspGluProTrpLysArg 820
Db 737 TGCCCCAGAAAGTTTGTCTGAACCTGTTTACATCAGTGTGGGAGCTGATGCCAAGAAACGG 796
QY 821 ProSerPheSerSerIleMetGluThrLeuLysProMetThr 834
Db 797 CCATCATTCAGCAATCATTTCAATCCTGGAGTCCATGTCA 838

RESULT 11
US-09-917-800A-1405
; Sequence 1405, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Blashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31

; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1405
; LENGTH: 2719
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 M15428
US-09-917-800A-1405
Alignment Scores:
Pred. No.: 2.5e-40 Length: 2719
Score: 475.50 Matches: 130
Percent Similarity: 53.26% Conservative: 74
Best Local Similarity: 33.94% Mismatches: 134
Query Match: 10.72% Indels: 45
DB: 10 Gaps: 13
US-09-904-389-2 (1-850) x US-09-917-800A-1405 (1-2719)
QY 474 LysAspArgAsnSerGlnLeuLeuAsnLysLysAlaAlaGlnLeuAsnThrGlnAspGly 493
Db 842 AGAGAAAGGGAAATGAATCTGGAACCTTAAGTGTACTCTTGAAGAAACAAAGGAAGAG 901
QY 494 LysSerGluGlnPheArgSerCysValAlaSerProTyrSerValGlnSerThrProPhe 513
Db 902 GATGCAATTGGAAGTCACAGTGAATCAGCCTCACCTTCAGCCCTGTCCAGCAGCCCC-- 958
QY 514 ValGluAsnValValProLeuSerHisIleSerHisIleGlySerGluAspSerGluHis 533
Db 959 ---AACAACTGAGCCCA----- 973
QY 534 LeuLeuAlaLeuSerHisProArgMetAspHisValAsnAsnLeuProPheValHisGly 553
Db 974 ---ACAGGCTGGTCCAGCCCAAAACCCCTGTGTCAGCACAAAGAGAGAGGGCGCCAGGA 1030
QY 554 SerGlnLeuIleArgLysProAsnGluLeuSerLeuGlyLeuGluAspLeuValIlePro 573
Db 1031 TCTGGGACCCAGGAAACAAACAAATTAGGCTCGTGGGCGAGAGATTCAAGTTATTAC 1090
QY 574 Trp-----ThrAspLeuAspLeuArgGluLysIleGlyAlaGlySerPheGly 589
Db 1091 TGGGAATAGAACCCAGTGAAGTGAATGCTGTCTACTCGGATTGGCTCGGCTCCTTTGGC 1150
QY 590 ThrValTyrArgGlyGluTrpHisGlySerAspValAlaValLysIleLeuThrGluGln 609
Db 1151 ACTGTGTACAAAGGGCAAGTGGCATGGA---GATGTTGCAGTAAAGATCCTAAAGTGCTT 1207
QY 610 AspPheHisProGluArgValAsnGluPheLeuArgGluValAlaIleMetLysSerLeu 629
Db 1208 GACCCAACTCCAGAGCAACTTCAGGCCCTTCAGGAACGAGGTGGCTGTTTGGCGAAACA 1267
QY 630 ArgHisProAsnIleValLeuPheMetGlyAlaValThrLysProProAsnLeuSerIle 649
Db 1268 CGGCATGTTAATATCTGCTGTTTCATGGGGTACATGACAAAG---GACAACTGGCGATT 1324
QY 650 ValThrGluTyrLeuSerArgGlySerLeuTyrArgLeuLeuHisLysSerGlyValLys 669

Db 1325 GTGACCCAGTGTGTGAAGGCAGCAGTCTCTACAAACACCTGCAT----- 1369

Qy 670 AspIleAspGluThrArg-----ArgIleAsnMetAlaPheAspValAla 684

Db 1370 ---GTCCAGGAGACCAATTCAGATGTTCCAGTAAATTGACATTGCCCGGCAGACAGCT 1426

Qy 685 LysGlyMetAsnTyrLeuHisArgArgAspProProIleValHisArgAspLeuLysSer 704

Db 1427 CAGGGAATGGACTATTACATGCAAGAAC-----ATCATCCACAGACATGAATCC 1480

Qy 705 ProAsnLeuValAspLysTyrThrValLysValCysAspPheGlyLeuSerArg 724

Db 1481 AACAATATATTCTCCATGAAGGCCTCAGGTGAAATCGGAGATTTTGGTTGGCAACA 1540

Qy 725 LeuLysAlaArgThrPheLeuSerSer-----LysSerAlaAlaGlyThrProGluTrp 742

Db 1541 GTGAAGTCGCGCTGGAGTGGTTCTCAGCAGGTTGAACAGCCCACTGGCTCTGTGCTGTGG 1600

Qy 743 MetAlaProGluValLeuArg-----AspGluProSerAsnGluLysSerAspVal 759

Db 1601 ATGGCCCCAGAAAGTAATCCGAATGCAGGATAACAACCCGTTCCAGTTCAGTCCGATGC 1660

Qy 760 TyrSerPheGlyValIleLeuTrpGluLeuAlaThrLeuGlnGlnProTrpCysAsnLeu 779

Db 1661 TACTCCTATGGCATTTGCTGTATGAGCTGATGACTGGGGAGCTTCCCTACTCCCAATC 1720

Qy 780 AsnProAla---GlnValValAlaAlaValGlyPheLysGlyLysArgLeuAspIlePro 798

Db 1721 AACAAACGAGACCAAGATCATCTTCATGGTGGCGCTGGGTACCGCTCCCAAGATCTTAGC 1780

Qy 799 ArgAspValAsn-----ProLysLeuAlaSerLeuIleValAla---CysTrpAlaAsp 815

Db 1781 AGGCTCTACAAGAACTGCCCAAGGCAATGAAGAGGTTGGTGGCTGACTGTGTGAAGAAA 1840

Qy 816 GluProTrpLysArgProSerPheSerSerIleMetGluThrLeuLysProMetThrLys 835

Db 1841 GTCAAGAAGAAAGGCCTTTGTTTCTCAGATCCTGTCTTCCATTGAGCTGCTTCAGCAC 1900

Qy 836 GlnAlaPro 838

Db 1901 TCTCTGCCG 1909

RESULT 12

US-10-440-341-6

Sequence 6, Application US/10440341

Publication No. US20030181413A1

GENERAL INFORMATION:

APPLICANT: RAPP, ULF

APP, HARALD

STORM, STEPHEN M.

TITLE OF INVENTION: RAF PROTEIN KINASE THERAPEUTICS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN, DARBY & CUSHMAN

STREET: 1100 NEW YORK AVE., N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/440,341

FILING DATE: 15-May-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/748,931

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: SCOTT, WATSON T.

REGISTRATION NUMBER: 26,581

REFERENCE/DOCKET NUMBER: 5683/82731

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-861-3067

TELEFAX: 202-822-0944

TELEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 2229 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-440-341-6

Alignment Scores:

Pred. No.: 8.07e-40 Length: 2229

Score: 469.50 Matches: 143

Percent Similarity: 51.24% Conservative: 84

Best Local Similarity: 32.28% Mismatches: 168

Query Match: 10.59% Indels: 51

DB: 12 Gaps: 16

US-09-904-389-2 (1-850) x US-10-440-341-6 (1-2229)

Qy 419 SerLeuAlaLysGlnTyrPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAla 438

Db 693 TCCTAGCAGAGACTGCCCTAACATCTGGATCATCCCTTCCGACCCGCTCGGACTCT 752

Qy 439 SerSerGlyAsnValValSerGlyLysAspAlaAlaPheSerVal---TyrGlnArgPro 457

Db 753 ATTGGGCCCCAAATTCTCACCAGTCCGTCCTCTCAAATCCCAATCCCAATCCACAGCCC 812

Qy 458 LeuAsnArgLysAspValAspGlyLysThrIleValValThrGlyAspLysAspArgAsn 477

Db 813 TTCCGACCAGCAGATGAAGATCATCGAAAT-----CAATTGGGCAACGAGACCGATCC 866

Qy 478 SerGlnLeuLeuAsnLysLysAlaAlaGlnLeuAsnThrGlnAspGly----- 493

Db 867 TCATCAGCTCCCAAT-----GTGCATATAAACACATAGAACCTGCAATTGAT 917

Qy 494 -----LysSerGluGlnPheArgSerCysValAlaSerProTyrSerValGlnSer 510

Db 918 GACTTGATTAGACACCAAGATTTCGTGGTGTGGAGGATCAACCACAGGTTTGTCTGCT 977

Qy 511 ThrPro-----PheValGluAsnValValProLeuSerHisIleSer 524

Db 978 ACCCCCTGCCTCATTACCTGGCTCACTAACTAAGTGAA-AGCCTTACAGAAATCTCC 1036

Qy 525 HisIleGlySerGluAspSerGluHisLeuLeuAlaLeuSerHisProArgMetAspHis 544

Db 1037 AGGACCTC-AGCGAGAAAGGAAGTCATCTT-----CATCCTCAGAAGACAGGA 1083

Qy 545 ValAsnAsnLeuProPheValHisGlySerGlnLeuIleArgLysProAsnGluLeuSer 564

Db 1084 ATCGAATGAAAACACCTTGGTAGACGGGACTCGAGT----- 1118

Qy 565 LeuGlyLeuGluAspLeuValIleProTrpThrAspLeuAspLeuArgGluLysIleGly 584

Db 1119 -----CATGATTGGGAGATTCTGATGGGCAGATTACAGTGGGACAAAGATTGGA 1169

Qy 585 AlaGlySerPheGlyThrValTyrArgGlyGluTrpHisGlySerAspValAlaValLys 604

Db 1170 TCTGGATCATTTGGAACAGTCTACAAGGGAAAGTGGCATGGT---GATGTGGCAGTGAAA 1226

Qy 605 IleLeuThrGluGlnAspPheHisProGluArgValAsnGluPheLeuArgGluValAla 624

Db 1227 ATGTTGAATGTGACAGCACCTACACCTCAGCAGTTACAAGCCTTCAAAATGAAGTAGGA 1286

Qy 625 IleMetLysSerLeuArgHisProAsnIleValLeuPheMetGlyAlaValThrLysPro 644

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Db 1287 GTACTCAGGAAAACACGACATGTGAATATCCTACTCTTTCATGGGCTATTCCACAAAG--- 1343
Qy 645 ProAsnLeuSerIleValThrGluTyrLeuSerArgGlySerLeuTyrArgLeuLeuHis 664
Db 1344 CCACAACTGGCTATTGTACCCAGTGGTGAGGGCTCCAGCTTGATCACCATCTCCAT 1403
Qy 665 LysSerGlyValLysAspIleAspGluThrArgArgIleAsnMetAlaPheAspValAla 684
Db 1404 ATCATTGAGACCAA---TTTGAGATGATCAAACTTATAGATATTCACGACAGACTGCA 1460
Qy 685 LysGlyMetAsnTyrLeuHisArgArgAspProProlleValHisArgAspLeuLysSer 704
Db 1461 CAGGCATGGATTACTTACACGCCAAGTCA-----ATCATCCACAGAGACCTCAAGAGT 1514
Qy 705 ProAsnLeuLeuValAspLysLysTyrThrValLysValCysAspPheGlyLeuSerArg 724
Db 1515 AATAATATATTCTTTCATGAAGACCTCACAGTAAATAATAGGTGATTTGGTCTAGCTACA 1574
Qy 725 LeuLysAlaArgThrPheLeuSerSer-----LysSerAlaAlaGlyThrProGluTrp 742
Db 1575 GTGAATCTCGATGGAGTGGGTCCCATCAGTTTGAACAGTTGTCTGGATCCATTTTGTGG 1634
Qy 743 MetAlaProGluValLeuArgAspGluProSerAsnGlu-----LysSerAspVal 759
Db 1635 ATGGCACAGAAAGTCATCAGAAATGCAAGATAAAATCCATACAGCTTTCAGTCAGATGTA 1694
Qy 760 TyrSerPheGlyValIleLeuTrpGluLeuAlaThrLeuGlnGlnProTrpCysAsnLeu 779
Db 1695 TATGCAATTGGAATTGTTCTGTATGAATTGATGACTGGACAGTTACCTTATTCAAACATC 1754
Qy 780 AsnProAla---GlnValValAlaAlaVal-----GlyPheLysGlyLysArgLeuAsp 796
Db 1755 AACAAACAGGACACAGATAATTTTATGGTGGGACGAGATACCTGTCTCCAGATCTCAGT 1814
Qy 797 IleProArgAspValAsnProLys---LeuAlaSerLeuIleValAlaCysTrpAlaAsp 815
Db 1815 AAGGTACGGAGTAACCTGTCCAAAGCCATGAAGAGATTAATGGCAGAGTGCTCAAAAAG 1874
Qy 816 GluProTrpLysArgProSerPheSerSerIleMetGluThrLeuLysProMetThrLys 835
Db 1875 AAAAGAGATGAGAGACCACCTCTTTCCCCAAATTCGCGCTCTATTGAGCTGCTGGCCCGC 1934
Qy 836 GlnAlaPro 838
Db 1935 TCATTGCCA 1943
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RESULT 13
US-10-057-550-89
; Sequence 89, Application US/10057550
; Publication No. US20030032607A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/057,550
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/506,073
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 09/143,214
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: PCT/US98/13961
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: US 08/888,982
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US 08/756,806
; PRIOR FILING DATE: 1996-11-26
; PRIOR APPLICATION NUMBER: PCT/US95/07111
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/250,856
; PRIOR FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 89
; LENGTH: 2510
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; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
US-10-057-550-89
Alignment Scores:
Pred. No.: 9.73e-40 Length: 2510
Score: 469.50 Matches: 143
Percent Similarity: 51.24% Conservative: 84
Best Local Similarity: 32.28% Mismatches: 168
Query Match: 10.59% Indels: 51
DB: 14 Gaps: 16
US-09-904-389-2 (1-850) x US-10-057-550-89 (1-2510)
Qy 419 SerLeuAlaLysGlnTyrPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAla 438
Db 974 TCCTTAGCAGAGACTGCCCTAAACATCTGGATCATCCCTTCCGCACCCGCCCTCGGACTCT 1033
Qy 439 SerSerGlyAsnValValSerGlyLysAspAlaAlaPheSerVal---TyrGlnArgPro 457
Db 1034 ATTGGGCCCAAAATTCTCACAGTCCGTCTCCTTCAAAATCCATTCCCAATCCACAGCCC 1093
Qy 458 LeuAsnArgLysAspValAspGlyLysThrIleValValThrGlyAspLysAspArgAsn 477
Db 1094 TTCCGACCAGCAGATGAAGATCATCGAAAT-----CAATTGGGCAACGAGACCGATCC 1147
Qy 478 SerGlnLeuLeuAsnLysLysAlaAlaGlnLeuAsnThrGlnAspGly----- 493
Db 1148 TCATCAGCTCCCAAT-----GTGCATATAAACACAAATAGAACCTGTCAATATTGAT 1198
Qy 494 -----LysSerGluGlnPheArgSerCysValAlaAlaSerProTyrSerValGlnSer 510
Db 1199 GACTTGATTAGACCAAGGATTTCGTGGTGATGGAGGATCAACCACAGGTTTGTCTGCT 1258
Qy 511 ThrPro-----PheValGluAsnValValProLeuSerHisIleSer 524
Db 1259 ACCCCCCCTGCCTCATTACCTGGTCACTAACTAACGTGAA-AGCCTTACAGAAATCTCC 1317
Qy 525 HisIleGlySerGluAspSerGluHisLeuLeuAlaLeuSerHisProArgMetAspHis 544
Db 1318 AGGACCTC-AGCGAGAAAGGAAGTCACTTT-----CATCCTCAGAAGACAGGA 1364
Qy 545 ValAsnAsnLeuProPheValHisGlySerGlnLeuIleArgLysProAsnGluLeuSer 564
Db 1365 ATCGAATGAAACACTTGGTAGCGGACTCGAGT----- 1399
Qy 565 LeuGlyLeuGluAspLeuValIleProTrpThrAspLeuAspLeuArgGluLysIleGly 584
Db 1400 -----GATGATTGGGAGATTCTCTGATGGGCAGATTACAGTGGGACAAAGATTGGA 1450
Qy 585 AlaGlySerPheGlyThrValTyrArgGlyGluTrpHisGlySerAspValAlaValLys 604
Db 1451 TCTGGATCATTTGGAAACAGTCTACAGGGAAGTGGCATGGT---GATGTGGCAGTGAAA 1507
Qy 605 IleLeuThrGluGlnAspPheHisProGluArgValAlaAsnGluPheLeuArgGluValAla 624
Db 1508 ATGTTGAATGTGACAGCACCTACACCTCAGCAGTTTACAAGCCCTTCAAAATGAAGTAGGA 1567
Qy 625 IleMetLysSerLeuArgHisProAsnIleValLeuPheMetGlyAlaValThrLysPro 644
Db 1568 GTACTCAGGAAACACGACATGTGAATATCTACTCTTTCATGGGCTATTCCACAAAG--- 1624
Qy 645 ProAsnLeuSerIleValThrGluTyrLeuSerArgGlySerLeuTyrArgLeuLeuHis 664
Db 1625 CCACAACTGGCTATTGTGTACCCAGTGGTGTGAGGGCTCCAGCTTGTATCACCATCTCCAT 1684
Qy 665 LysSerGlyValLysAspIleAspGluThrArgArgIleAsnMetAlaPheAspValAla 684
Db 1685 ATCATTGAGACCAA---TTTGAGATGATCAAACTTATAGATATTGACGACAGACTGCA 1741
Qy 685 LysGlyMetAsnTyrLeuHisArgArgAspProProlleValHisArgAspLeuLysSer 704
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Db 1742 CAGGGCATGGATTACTTACACGCCAAGTCA-----ATCATCCACAGAGACCTCAAGAGT 1795

Qy 705 ProAsnLeuLeuValAspLysLysTyrThrValLysValCysAspPheGlyLeuSerArg 724

Db 1796 AATAATATATTCTTCATGAAGACCTCACAGTAAATAAGGTGATTTTGGTCTAGCTACA 1855

Qy 725 LeuLysAlaArgThrPheLeuSerSer-----LysSerAlaAlaGlyThrProGluTrp 742

Db 1856 GTGAAATCTCGATGGAGTGGGTCCCATCAGTTTGAACAGATTGTCTGGATCCATTTTGTGG 1915

Qy 743 MetAlaProGluValLeuArgAspGluProSerAsnGlu-----LysSerAspVal 759

Db 1916 ATGGCACCAAGATCATCAGAAATGCAAGATAAAATCCATACAGCTTTTCAGTCAGATGTA 1975

Qy 760 TyrSerPheGlyValIleLeuTrpGluLeuAlaThrLeuGlnGlnProTrpCysAsnLeu 779

Db 1976 TATGCATTGGGATTTCTGTATGAATTGATGACTGGACAGTTACCTTATTCAAAACATC 2035

Qy 780 AsnProAla---GlnValValAlaAlaVal-----GlyPheLysGlyLysArgLeuAsp 796

Db 2036 AACAAACAGGACCATGATAATTTTATGGTGGGACGAGGATACCTGTCTCCAGATCTCAGT 2095

Qy 797 IleProArgAspValAsnProLys---LeuAlaSerLeuIleValAlaCysTrpAlaAsp 815

Db 2096 AAGGTACGGAGTAACACTGTCCAAAGGCCATGAAGAGATTATGGCAGAGTGCCTCAAAAAG 2155

Qy 816 GluProTrpLysArgProSerPheSerSerIleMetGluThrLeuLysProMetThrLys 835

Db 2156 AAAAGAGATGAGAGACCACACTCTTCCCAAAATTCGCGCTCTATTGAGCTGCTGGCCCGC 2215

Qy 836 GlnAlaPro 838

Db 2216 TCATTGCCA 2224

RESULT 14

US-10-173-225B-67

Sequence 67, Application US/10173225B

Publication No. US20030119769A1

GENERAL INFORMATION:

APPLICANT: Monia, Brett P.

TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression

FILE REFERENCE: ISPH-0665

CURRENT APPLICATION NUMBER: US/10/173,225B

CURRENT FILING DATE: 2002-12-06

PRIOR APPLICATION NUMBER: US 10/057,550

PRIOR FILING DATE: 2002-01-25

PRIOR APPLICATION NUMBER: US 09/143,214

PRIOR FILING DATE: 1998-08-28

PRIOR APPLICATION NUMBER: PCT/US98/13961

PRIOR FILING DATE: 1998-07-06

PRIOR APPLICATION NUMBER: US 08/888,982

PRIOR FILING DATE: 1997-07-07

PRIOR APPLICATION NUMBER: US 08/756,806

PRIOR FILING DATE: 1996-11-26

PRIOR APPLICATION NUMBER: PCT/US95/07111

PRIOR FILING DATE: 1995-05-31

PRIOR APPLICATION NUMBER: US 08/250,856

PRIOR FILING DATE: 1994-05-31

NUMBER OF SEQ ID NOS: 109

SEQ ID NO 67

LENGTH: 2510

TYPE: DNA

ORGANISM: homo sapiens

US-10-173-225B-67

Alignment Scores:

Pred. No.:	9,73e-40	Length:	2510
Score:	469.50	Matches:	143
Percent Similarity:	51.24%	Conservative:	84
Best Local Similarity:	32.28%	Mismatches:	168
Query Match:	10.59%	Indels:	51
DB:	14	Gaps:	16

US-09-904-389-2 (1-850) x US-10-173-225B-67 (1-2510)

Qy 419 SerLeuAlaLysGlnTyrPheLeuAspSerGlnSerLeuAsnLeuValPheAspGluAla 438

Db 974 TCCTTAGCAGAGACTGCCCTAACATCTGGATCATCCCTTCGCACCCGCTCGGACTCT 1033

Qy 439 SerSerGlyAsnValValSerGlyLysAspAlaAlaPheSerVal---TyrGlnArgPro 457

Db 1034 ATTGGGCCCCAAATTCTCACCAGTCGCTCTCCTTCAAAATCCATTCCAATTCCACAGCCC 1093

Qy 458 LeuAsnArgLysAspValAspGlyLysThrIleValValThrGlyAspLysAspArgAsn 477

Db 1094 TTCCGACCAGCAGATGAAGATCATCGAAAT-----CAATTGGGCAACGAGACCGATCC 1147

Qy 478 SerGlnLeuLeuAsnLysLysAlaAlaGlnLeuAsnThrGlnAspGly----- 493

Db 1148 TCATCAGCTCCCAAT-----GTGCATATAAACACACATAGAACCTGTCAATATTGAT 1198

Qy 494 -----LysSerGluGlnPheArgSerCysValAlaSerProTyrSerValGlnSer 510

Db 1199 GACTTGATTAGAGACCAAGGATTTCTGGTGATGGAGGATCAACCACAGGTTTGTCTGCT 1258

Qy 511 ThrPro-----PheValGluAsnValValProLeuSerHisIleSer 524

Db 1259 ACCCCCCCTGCCTCATTTACCTGGCTCACTAACTAAGTGAA-AGCCTTACAGAAATCTCC 1317

Qy 525 HisIleGlySerGluAspSerGluHisLeuLeuAlaLeuSerHisProArgMetAspHis 544

Db 1318 AGGACCTC-AGCGAGAAAGGAAGTCACTTT-----CATCCTCAGAAGACAGGA 1364

Qy 545 ValAsnAsnLeuProPheValHisGlySerGlnLeuIleArgLysProAsnGluLeuSer 564

Db 1365 ATCGAATGAAACACACTTGGTAGACGGGACTCGAGT----- 1399

Qy 565 LeuGlyLeuGluAspLeuValIleProTrpThrAspLeuAspLeuArgGluLysIleGly 584

Db 1400 -----GATGATTGGGAGATTCTCTGATGGGCAGATTACAGTGGGACAAAGATTGGA 1450

Qy 585 AlaGlySerPheGlyThrValTyrArgGlyGluTrpHisGlySerAspValAlaValLys 604

Db 1451 TCTGGATCATTTTGGAAACAGTCTACAAGGAAAGTGGCATGGT---GATGTGGCAGTGAAA 1507

Qy 605 IleLeuThrGluGlnAspPheHisProGluArgValAsnGluPheLeuArgGluValAla 624

Db 1508 ATGTTGAATGTGACACACCTACACCTCAGCAGTTACAAGCCCTTCAAAAATGAAGTAGGA 1567

Qy 625 IleMetLysSerLeuArgHisProAsnIleValLeuPheMetGlyAlaValThrLysPro 644

Db 1568 GTACTCAGGAAAAACACGACATGTGAATATCTACTCTTTCATGGGCTATTCACCAAAG--- 1624

Qy 645 ProAsnLeuSerIleValThrGluTyrLeuSerArgGlySerLeuTyrArgLeuLeuHis 664

Db 1625 CCACAACTGGCTATTGTACCCAGTGTGTGAGGGCTCCAGCTTGTATCACCATCTCCAT 1684

Qy 665 LysSerGlyValLysAspIleAspGluThrArgArgIleAsnMetAlaPheAspValAla 684

Db 1685 ATCATTGAGACCACAA---TTTGAGATGATCAAACTTATAGATATTGCACGACAGACTGCA 1741

Qy 685 LysGlyMetAsnTyrLeuHisArgArgAspProIleValHisArgAspLeuLysSer 704

Db 1742 CAGGGCATGGATTACTTACACGCCCAAGTCA-----ATCATCCACAGACCTCAAGAGT 1795

Qy 705 ProAsnLeuLeuValAspLysLysTyrThrValLysValCysAspPheGlyLeuSerArg 724

Db 1796 AATAATATATTTCTTCATGAAGACCTCACAGTAAATAAGTGGTATTGGTCTAGCTACA 1855

Qy 725 LeuLysAlaArgThrPheLeuSerSer-----LysSerAlaAlaGlyThrProGluTrp 742

Db 1856 GTGAAATCTCGATGGAGTGGGTCCCATCAGTTTGAACAGATTGTCTGGATCCATTTTGTGG 1915

Qy 743 MetAlaProGluValLeuArgAspGluProSerAsnGlu-----LysSerAspVal 759

Db 1916 ATGGCACCAAGATCATCAGAAATGCAAGATAAAATCCATACAGCTTTTCAGTCAGATGTA 1975

QY 760 TyrSerPheGlyValIleLeuTrpGluLeuAlaThrLeuGlnProTrpCysAsnLeu 779
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1976 TATGCATTGGGATTGTTCTGTATGAATTGATGACTGGACAGTTACCTTATTCAAACATC 2035
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 780 AsnProAla--GlnValValAlaAlaVal-----GlyPheLysGlyLysArgLeuAsp 796
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 2036 AACACAGGACCCAGATAAATTTTATGGTGGACGAGGATACCTGTCTCCAGATCTCAGT 2095
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 797 IleProArgAspValAsnProLys---LeuAlaSerLeuIleValAlaCysTrpAlaAsp 815
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 2096 AAGTACGGAGTAACCTGTCCAAAGCCATGAAGAGATTAAATGGCAGAGTGCCTCAAAAAG 2155
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 816 GluProTrpLysArgProSerPheSerSerIleMetGluThrLeuLysProMetThrLys 835
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 2156 AAAAGAGATGAGAGACCACTCTTTCCCAAAATCTCGCCTCTATTGAGCTGCTGGCCCGC 2215
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QY 836 GlnAlaPro 838
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 2216 TCATTGCCA 2224
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :

RESULT 15
US-10-210-120-86
; Sequence 86, Application US/10210120
; Publication No. US20030175736A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Rubin, Mark A.
; APPLICANT: Sreekumar, Arun
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; FILE REFERENCE: UM-07221
; CURRENT APPLICATION NUMBER: US/10/210,120
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/309,581
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/334,468
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 86
; LENGTH: 3435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-120-86

Alignment Scores:
Pred. No.: 3,34e-39 Length: 3435
Score: 466.50 Matches: 113
Percent Similarity: 53.42% Conservative: 43
Best Local Similarity: 38.70% Mismatches: 111
Query Match: 10.52% Indels: 25
DB: 12 Gaps: 7

US-09-904-389-2 (1-850) x US-10-210-120-86 (1-3435)

QY 560 ProAsnGluLeuSerLeuGlyLeuGluAspLeuValIleProTrpThrAspLeuAspLeu 579
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 538 CCCGCGGCCTCCAGCTGCCCCAGGAG-----ATCCCTTCCACGAGCTGCAGCTA 588
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 580 ArgGluLysIleGlyAlaGlySerPheGlyThrValTyArgGlyGluTrpHisGlySer 599
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 589 GAGGAGATCATCGGTGTGGGGGCTTTTGGCAAGGTCTATCGGSCCCTGTGGCGTGGCGAG 648
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 600 AspValAlaValIysIleLeuThrGluGlnAspPheHisProGluArg----- 615
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 649 GAGGTGGCAGTCAAGCCGCCCGG-----CTGGACCTTGAGAAGGACCCGCGAGTG 699
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 616 ---ValAsnGluPheLeuArgGluValAlaIleMetLysSerLeuArgHisProAsnIle 634
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 700 ACAGCGGAGCAGGTGTGCCAGGAAGCCCGGCTCTTTGGAGCCCTGCAGCACCCCAACATA 759
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 635 ValLeuPheMetGlyAlaValThrLysProAsnLeuSerIleValThrGluTyLeu 654
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :

Db 760 ATTGCCCTTAGGGGCGCTGCCTCAACCCCCCACACCTCTGCTAGTGATGGAGTATGCC 819
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 655 SerArgGlySerLeuTyArgLeuLeuHisLysSerGlyValLysAspIleAspGluThr 674
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 820 CGGGGTGGTGCACTGACAGGGTGCTG-----GCAGGTCCGGGTGCCACCTCAC 870
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 675 ArgArgIleAsnMetAlaPheAspValAlaLysGlyMetAsnTyLeuHisArgArgAsp 694
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 871 GTGTGGTCAACTGGGCTGTGCAGGTGGCCCGGGCATGAACCTACACACATGATGCC 930
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 695 Pro---ProIleValHisArgAspLeuLysSerProAsnLeuValAspLysLysTy 713
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 931 CCTGTGCCCATCATCCACCGGACCTCAAGTCCATCAACATCCTGATCCTGGAGGCCATC 990
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 714 -----ThrValLysValCysAspPheGlyLeuSerArgLeu 725
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 991 GAGAACCAACCTCGCAGACACGGTGTCTCAAGATCACGGACTTCGGCCTCGCCCGCAG 1050
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 726 LysAlaArgThrPheLeuSerSerLysSerAlaAlaGlyThrProGluTrpMetAlaPro 745
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1051 TGGCACAGACC-----ACCAAGATGAGCGCTCGGGGACCTACGCCCTGGATGGCGCG 1104
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 746 GluValLeuArgAspGluProSerAsnGluLysSerAspValTySerPheGlyValIle 765
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1105 GAGGTATCCGCTCTCTCCCTCTTCTCCAAAGCAGTGTCTGGAGCTTCGGGTGCTG 1164
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 766 LeuTrpGluLeuAlaThrLeuGlnGlnProTrpCysAsnLeuAsnProAlaGlnValVal 785
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1165 CTGTGGGAGCTGCTGACGGGGAGGTCCCTACCGTGAGATCGACGCCCTTGGCCGTGGCG 1224
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 786 AlaAlaValGlyPheLysGlyLysArgLeuAspIleProArgAspValAsnProLysLeu 805
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1225 TATGGCGTGGCTATGAATAAGCTGACGCTGCCCATTCCTCCACGTGCCCGGAGCCCTTT 1284
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 806 AlaSerLeuIleValAlaCysTrpAlaAspGluProTrpLysArgProSerPheSerSer 825
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1285 GCCCGCCTCCTGGAGGAATGTGGGACCCAGACCCCCACGGGGCCGAGATTTCGGTAGC 1344
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 826 IleMetGluThrLeuLysProMetThrLysGlnAla 837
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1345 ATCTTGAAGCGGCTTGAAGTCATCGAACAGTCAGCC 1380
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :

Search completed: October 24, 2003, 05:09:58
Job time : 1001 secs

Db 61 WDPGGGGGHRLLNQNPNRVGNMNYASSLGLQROSSGSGSFGESSLGSDYIMPTLS-AAAN 119
QY 104 EINALEYILDDDFRV-----MKAVGSGG-SSGKSWAQOTEESFOLQOPLVLRL 150
Db 120 EIESVGFPQDDGFRLGFGGGGDLRIQMAADSAGGSSGKSWAQOTEESYQLQALALRL 179
QY 151 SSDXTCADDPNFMDDPIDEAALRSLISISAEASHRFWNGCMSYLEKVPDGFYLHGM DP 210
Db 180 SSEATCADDPNFDLPVDESALRTSPSSAETVSHRFWNGCLSYDKVPDGFYMNGLDP 239
QY 211 YVWSLCTNLQEDGRIPSFESLKTVDSSIGSIEVVLIDRHSDASLKELOQNRVHNISSCV 270
Db 240 YIWTLCIDLHESGRIPSIESLRAVDSGVDSLEAIIIVDRSDPAFKELNHRVHDISCSI 299
QY 271 TTKEVADHIAKLVNHLGGSVSEGEDDLVSAWKECSDDLKECLGSAVIFLCSLSVGLCRH 330
Db 300 TTKEVVDQLAKLICNRMGGPVIMGEDELVPMWKECIDGLKE-IFKVVPVIGLSVGLCRH 358
QY 331 RALLFKVLADSIDLPCRIAGCKYCTRDDASSCLVRFGLDREYLIDLIGRPGCLCQPD SL 390
Db 359 RALLFKVLADIIDLPCRIAGCKYCNRDDAASCLVRFGLDREYLDLVGKPGHLWEPSL 418
QY 391 LNPSSISISSPLRFPRLKPIESTIDFRSLAKQYFLDSQSLNLFVDEASSGNVVGKDA A 450
Db 419 LNPSSISISSPLRFPRLKPIESTIDFRSLAKQYFSDSQSLNLFVDPASD-----DMG 471
QY 451 FSVYQRP LN RKVDGKTIIVVTGDKDRNSQLLNKKAQLNTQDGKSEQFRSCVSPYSVQS 510
Db 472 FSNFHRQYDNPFGGENDALAENG-----GS 496
QY 511 TPFEVENVVPLSHISHIGSEDSHLLALSHPRMDHVNLPFVHGSQ LIRKPNELSLGLEDL 570
Db 497 LPPSANMPP-----QNMVRASNQIEAAPNAPPISQVPNRRANRELGLDGD DM 544
QY 571 VIPWTDLDLREKIGAGSFGTVYRGGEWHGSDVAVKILTEQDFHPERVNEFLREVAIMKSLR 630
Db 545 DIPWCDLNIKEKIGAGSFGTVHRAEWHGSDVAVKILMEQDFHAERVNEFLREVAIMKRLR 604
QY 631 HPNIVLFMGAVTKPPNLSIVTEYLSRGSLYRLHLHKSQVKD-IDETRRINMAFDVAKGMNY 689
Db 605 HPNIVLFMGAVTQPPNLSIVTEYLSRGSLYRLHLHKSAREQLDERRRLSMAYDVAKGMNY 664
QY 690 LHRRDPPIVHRDLKSPNLLVDKKTVKVCDFGLSRLKARTFLSSKSAAGTPEWMAPEVLR 749
Db 665 LHRNPPPIVHRDLKSPNLLVDKKTVKVCDFGLSRLKASTFLSSKSAAGTPEWMAPEVLR 724
QY 750 DEPSNEKSDVYSGVILWELATLQOPWCNLPNPAQVVAAGVFGKGRLLDIPRDVNPKLASLI 809
Db 725 DEPSNEKSDVYSGVILWELATLQOPWCNLPNPAQVVAAGVFGKGRLLDIPRNLPQVAAII 784
QY 810 VACWADEPWKRPSFSSIMETLKPMTKQAPPQQRSD 845
Db 785 EGCWTNEPWKRPSFATIMDLLRPLIKSAVPPENRSD 820

RESULT 2
US-08-003-311B-2
; Sequence 2, Application US/08003311B
; Patent No. 5444166
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene
; TITLE OF INVENTION: Constitutive Triple Response Gene
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
; ADDRESSEE: No. 5444166ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.

ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/003,311B
; FILING DATE: January 12, 1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/928,464
; FILING DATE: August 10, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lori Y. Beardsell
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: UPN-1108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 821 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-003-311B-2

Query Match 61.8%; Score 2742.5; DB 1; Length 821;
Best Local Similarity 62.3%; Pred. No. 3.2e-237;
Matches 546; Conservative 99; Mismatches 144; Indels 87; Gaps 14;

QY 1 MEMGRRSDYSLLSQIPDEEVG---TGASTSFYDSVAA-----GGNVIKGRTDR-VFD 49
Db 1 MEMGRRSNYTLSSQFSDDQVSVSVTGAPPHPHYDSLSENRSNHNSTGCKAKAERGGFD 60
QY 50 WD---GSGDRLNTQAYRIG-NLY-SWIGLQRHSSGSSYDDSSLSDDYIAPTLSNPAAN 103
Db 61 WDPSGGGGGHRLLNQNPNRVGNMNYASSLGLQROSSGSGSFGESSLGSDYIMPTLS-AAAN 119
QY 104 EINALEYILDDDFRV-----MKAVGSGG-SSGKSWAQOTEESFOLQOPLVLRL 150
Db 120 EIESVGFPQDDGFRLGFGGGGDLRIQMAADSAGGSSGKSWAQOTEESYQLQALALRL 179
QY 151 SSDXTCADDPNFMDDPIDEAALRSLISISAEASHRFWNGCMSYLEKVPDGFYLHGM DP 210
Db 180 SSEATCADDPNFDLPVDESALRTSPSSAETVSHRFWNGCLSYDKVPDGFYMNGLDP 239
QY 211 YVWSLCTNLQEDGRIPSFESLKTVDSSIGSIEVVLIDRHSDASLKELOQNRVHNISSCV 270
Db 240 YIWTLCIDLHESGRIPSIESLRAVDSGVDSLEAIIIVDRSDPAFKELNHRVHDISCSI 299
QY 271 TTKEVADHIAKLVNHLGGSVSEGEDDLVSAWKECSDDLKECLGSAVIFLCSLSVGLCRH 330
Db 300 TTKEVVDQLAKLICNRMGGPVIMGEDELVPMWKECIDGLKE-IFKVVPVIGLSVGLCRH 358
QY 331 RALLFKVLADSIDLPCRIAGCKYCTRDDASSCLVRFGLDREYLIDLIGRPGCLCQPD SL 390
Db 359 RALLFKVLADIIDLPCRIAGCKYCNRDDAASCLVRFGLDREYLDLVGKPGHLWEPSL 418
QY 391 LNPSSISISSPLRFPRLKPIESTIDFRSLAKQYFLDSQSLNLFVDEASSGNVVGKDA A 450
Db 419 LNPSSISISSPLRFPRLKPIESTIDFRSLAKQYFSDSQSLNLFVDPASD-----DMG 471
QY 451 FSVYQRP LN RKVDGKTIIVVTGDKDRNSQLLNKKAQLNTQDGKSEQFRSCVSPYSVQS 510
Db 472 FSNFHRQYDNPFGGENDALAENG-----GS 496
QY 511 TPFEVENVVPLSHISHIGSEDSHLLALSHPRMDHVNLPFVHGSQ LIRKPNELSLGLEDL 570
Db 497 LPPSANMPP-----QNMVRASNQIEAAPNAPPISQVPNRRANRELGLDGD DM 544
QY 571 VIPWTDLDLREKIGAGSFGTVYRGGEWHGSDVAVKILTEQDFHPERVNEFLREVAIMKSLR 630

Db 545 DIPWCDLNKEKIGAGSGFTVHRAEWHGSDVAVKILMEQDFHAERVNEFLREVAIMKRLR 604
QY 631 HPNIVLFMGAVTKPPNLSIVTEYLSRGSGLYRLLLHKSGVKD-IDETRRINNAFDVAKGMNY 689
Db 605 HPNIVLFMGAVTQPPNLSIVTEYLSRGSGLYRLLLHKSGAREQDERRRLSMAYDVAKGMNY 664
QY 690 LHRRDPPVHRDLKSPNLLVDKKTIVKVCDFGLSRLKARTFLSSKSAAGTPEWMAPEVLR 749
Db 665 LHNRNPPVHRDLKSPNLLVDKKTIVKVCDFGLSRLKASTFLSSKSAAGTPEWMAPEVLR 724
QY 750 DEPSNEKSDVYSFGVILWELATLQOPWCNLPNPAQVVAAGVFGKGRLDIPRDVNPKLASLI 809
Db 725 DEPSNEKSDVYSFGVILWELATLQOPWCNLPNPAQVVAAGVFGKGRLEIPRNLNPQVAAII 784
QY 810 VACWADEPWKRPSFSSIMETLKPMTKQAPPQQSRD 845
Db 785 EGCWTNEPWKRPSFATIMDLLRPLIKSAVPPPNRSD 820

RESULT 3

US-08-261-432-2
; Sequence 2, Application US/08261432
; Patent No. 5602322
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene
; TITLE OF INVENTION: and Mutations
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
; ADDRESSEE: No. 5602322ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/261,432
FILING DATE: June 17, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/003,311
FILING DATE: January 12, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: UPN-1864

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 821 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-261-432-2

Query Match 61.8%; Score 2742.5; DB 1; Length 821;
Best Local Similarity 62.3%; Pred. No. 3.2e-237;
Matches 546; Conservative 99; Mismatches 144; Indels 87; Gaps 14;

QY 1 MEMPGRRSDYSLLSQIPDEEVG---TGASTSFVDSVAA-----GGNVIKGRDTR-VFD 49
Db 1 MEMPGRRSNYTLTSQFSDQVSVSVTGAPPPHYDSSLSENRSNHSNGTGKAKAERGQGD 60

QY 50 WD---GSGDHRINTQAYRIG-NLY-SWIGLQRHSSGSSYDDSSLSDDYAYPTLSNPAAN 103
Db 61 WDPSSGGGGDHRLLNNQPNRVGNMNYASSLGLQRQSSGSGSGESSLSGDYMPILS-AAAN 119
QY 104 EINALLEYILDDDFRV-----MKAVGSGG-SSGSKSWAQOOTESFQLOQPLVLR 150
Db 120 EIESVGFPQDDGFRLLFGGGGGLRIQMAADSAGSSSSGSKSWAQOOTESYQLOLALRL 179
QY 151 SSDXTCADDPNEMDPIPEAALRSLSISABAIASHRFVWNGCMSYLEKVPDGGFYLLHGMDP 210
Db 180 SSEATCADDPNFDVPDESALRTSPSSAETVSHRFVWNGCLSYDKVPDGGFYMMNGLDP 239
QY 211 YVWSLCTNLQEDGRIPSEFSLKTVDSISGSSIEVLIDRHSDASLKLQNRVHNISSCV 270
Db 240 YIWTLCIDLHESGRIPSIESLRAVDSGVDSSLEAIIIVDRSDPAFKELHNRVHDISCSCI 299
QY 271 TTKEVADHIAKLVNHLGGSVSEGEDDLVSAWKECSDDLKECLGSAPIPLCSLSVGLCRH 330
Db 300 TTKEVWDQAKLICNRMGGPVIIMGEDELVPMWKECIDGLKE-IFKVVVPIGSLSVGLCRH 358
QY 331 RALLFKVLADSIDLPCRIAGCKYCTRDDASSCLVRFGLDREYLDLIGRPGCLCQPDLSL 390
Db 359 RALLFKVLADIIDLPCRIAGCKYCNRDDAASCLVRFGLDREYLDLVGKPGHLWEPSL 418
QY 391 LNGPSSISISSPLRPPRLPIESTIDFRSLAKQYFLDSQSLNLFVDEASSGNVVGKDA 450
Db 419 LNGPSSISISSPLRPPRPKPEPAVDFFLLAKQYFSDSQSLNLFVDFPASP-----DMG 471
QY 451 FSVYQRPNLNRKVDGKTIIVTGDKNRSQNLNKKAAQLNTQDGKSEQFRSCVASPYSVQS 510
Db 472 FSMFHRQYDNPGGENDALAENG-----GS 496
QY 511 TPVENVWPLSHISHIGSEDSEHLLALSHPRMDHVNNLFPVHGSQLIRKPNELSLGLEDL 570
Db 497 LPFSANMPP-----QNMNRASNQIEAAPMNAPPISQVPVNRANRELGLDGDMM 544
QY 571 VIPWTDLDLREKIGAGSGFTVYRGWGHGSDVAVKILTEQDFHPRVNEFLREVAIMKSLR 630
Db 545 DIPWCDLNKEKIGAGSGFTVHRAEWHGSDVAVKILMEQDFHAERVNEFLREVAIMKRLR 604
QY 631 HPNIVLFMGAVTKPPNLSIVTEYLSRGSGLYRLLLHKSGVKD-IDETRRINNAFDVAKGMNY 689
Db 605 HPNIVLFMGAVTQPPNLSIVTEYLSRGSGLYRLLLHKSGAREQDERRRLSMAYDVAKGMNY 664
QY 690 LHRRDPPVHRDLKSPNLLVDKKTIVKVCDFGLSRLKARTFLSSKSAAGTPEWMAPEVLR 749
Db 665 LHNRNPPVHRDLKSPNLLVDKKTIVKVCDFGLSRLKASTFLSSKSAAGTPEWMAPEVLR 724
QY 750 DEPSNEKSDVYSFGVILWELATLQOPWCNLPNPAQVVAAGVFGKGRLDIPRDVNPKLASLI 809
Db 725 DEPSNEKSDVYSFGVILWELATLQOPWCNLPNPAQVVAAGVFGKGRLEIPRNLNPQVAAII 784
QY 810 VACWADEPWKRPSFSSIMETLKPMTKQAPPQQSRD 845
Db 785 EGCWTNEPWKRPSFATIMDLLRPLIKSAVPPPNRSD 820

RESULT 4

PCT-US93-07347-2

; Sequence 2, Application PC/TUS9307347
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene and
; TITLE OF INVENTION: Mutations
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
; ADDRESSEE: Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.

	Query Match	26.9%;	Score 1191.5;	DB 3;	Length 263;
	Best Local Similarity	84.4%;	Pred. No. 9.7e-99;		
	Matches 222; Conservative	25;	Mismatches 15;	Indels 1;	Gaps 1;
Qy	572 IPWTDLDLREKIGAGSGFTVYRGEGHGSDDAVAKILTEQDFHPERVNEFLREVAIMKSIRH	631			
Dd	1 IPWCDDLNIKEKIGAGSGFTVHRAEWHGSDAVAKILMEQDFAHERVNEFLREVAIMKRLRH	60			
Qy	632 PNIVLFMGAVTKPPNLSIVTEYLSRGLSYRLHLHKSGVKD-IDETRINNAFADVAKGMNYL	690			
Dd	61 PNIVLFMGAVTQPNNLSIVTEYLSRGLSYRLHLHKSGAREQLDEPRLRLSMAYDVAKGMNYL	120			


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; CURRENT FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 09/390,425
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: US08/752,345
; PRIOR FILING DATE: 1996-11-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 263
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (1)...(263)
US-09-566-906-5

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Query Match	26.9%;	Score 1191.5;	DB 4;	Length 263;
Best Local Similarity	84.4%;	Pred. No. 9.7e-99;		
Matches 222:	Conservative	25;	Mismatches 15;	Indels 1;
				Gaps 1;

Qy	572	IPWTDLDLREKIGAGSFGTVYRGEGWHGSDVAVKILTEQDFHPERVNEFLREVAIMKSLRH	631
Db	1	IPWCDLNIKEKIGAGSFGTVHRAEWHGSDVAVKILMEQDFHAERVNEFLREVAIMKRLRH	60
Qy	632	PNIVLFMGAVTKPPNLSIVTEYLSRGSLYRLLLHKSGVKD-IDETRRINMAFDVAKGMNYL	690
Db	61	PNIVLFMGAVTQPPNLSIVTEYLSRGSLYRLLLHKSGAREQLDERRRLSMAYDVAKGMNYL	120
Qy	691	HRRDPPIVHRDLKSPNLLVDKKYTVKVCDFGLSRLKARTFLSSKSAAGTPENWMAPEVLRD	750
Db	121	HNRNPPIVHRDLKSPNLLVDKKYTVKVCDFGLSRLKASTFLSSKSAAGTPENWMAPEVLRD	180
Qy	751	EPSNEKSDVYSFGVILWELATLQOPWCNLPNPAQVVAAGVFGKGRLDIPRDVNPKLASLIV	810
Db	181	EPSNEKSDVYSFGVILWELATLQOPWGNLPNPAQVVAAGVFKCKRLEIPRNLNPQVAAIIE	240
Qy	811	ACWADEPWKRPSFSSIMETLKPM	833
Db	241	GCWTNEPWRKPSFATIMDLRLPL	263

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RESULT 9
US-09-221-235-5
; Sequence 5, Application US/09221235
; Patent No. 6043040
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,235
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-235-5

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Query Match	11.4%;	Score 504.5;	DB 3;	Length 455;
Best Local Similarity	40.9%;	Pred. No. 1.2e-36;		
Matches 112:	Conservative	41;	Mismatches 106;	Indels 15;
				Gaps 4;

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QY 564 SLGLEDLVIPWTDLDLREKIGAGSGFTGYRGEWHGSD--VAVKILTEQDFHPERVNEFLR 621
    ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 3 SLGASFVQIKFDDLQFFENC GGSGGSGFCGYRAKWI SQDKVEAVAKLLKIE-----K 52

QY 622 EVAIMKSLRHPNIVLFMGAVTKPPNLSITVEYLSRGSGLYRLHLHKSQVKDIDETRINWAF 681
    ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 53 FAEILSVLSHRNIIOFYGVILEPPNYGIIVTEYASLGSLDYINSRSEEMDMDHMTWAT 112

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QY	682	DVAKGMNYLHRRDP - PIVHRDLKSPNLLVDKKYTVKVCDFGLSRLKARTFLSSKSAAGTP	740
		: : : :	
Db	113	DVAKGMHYLHMEAPVKVIHRDLKSRNVVIAADGVLKICDFGASRFHNHT -- THMSLVGT	170
		: : : :	
QY	741	EWMapeVLrDEPSNEKSdYVSFGvILwELATlQPWCNLnPAQVAAVGfKGkRLDIPRD	800
		: : : :	
Db	171	PWMAPEVIQSLPVSETCTDYSGVVLWEMLTRVPFFKGLEGLQVAWLVEKXERLTIPSS	230
		: : : :	
QY	801	VNPKLASLIACWADEPWKRPPSPSSIMETLKPMT	834
		: : : :	
Db	231	CPRSpaELLHOCWEADAkRPsfFKoIISILESMS	264
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RESULT 10
US-09-221-928-5
; Sequence 5, Application US/09221928
; Patent No. 6121030
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,928
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-928-5

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Query Match 11.4%; Score 504.5; DB 3; Length 455;
Best Local Similarity 40.9%; Pred. No. 1.2e-36;
Matches 112; Conservative 41; Mismatches 106; Indels 15; Gaps 4;

622	EVAIMKSLRHPNIVLFMGAVTKPPNLSIVTEYLSRSLYRLHLHKS	GVKDI	DETRRINMAF	681
53	EAEILSVLSHRNIIQFYGVILEPENYGI	VT	EYASLSGLYDYINSNRSEEMD	HIMTWAT
682	DVAKGMNYLHRRDP - PIVHRDLKSPNLLVDK	KYTVK	CD	FGLSRLKARTFLSSKSAAGTP
113	DVAKGMHYLHMEAPVKVIHRDLKSRNVVIA	DGVLK	ICD	F
741	EWMAPEVLRDEPSNEKSDVYSFGVILWELATLQ	Q	PWCNLP	AAQVVAAGVFGKGRDIPRD
171	PWMAPEVIQSLPVSETCDTYSYGVVLWEMLT	REVP	F	KGLEGLQVAWL
801	VNPKLASLIVACWADEPWKRPSFSSIMETL	KPMT	834	
231	CPRSFAELLHOCWEADAKRPSFKOJISILES	MS	264	

RESULT 11
US-09-221-527-5
; Sequence 5, Application US/09221527
; Patent No. 6146832
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,527
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5

Db 3 SLGASFVQIKFDDDLQFFENC GGSGFSGVYRAKWISQDKEVAVKLLKIE-----K 52

QY 622 EVAIMKSLRHPNIVLFMGAVTKPPNLSIVTEYLSRGSYRLHLHKSQVXKIDETRRINMAF 681

Db 53 EAEILSVLSHRNIIQFYGVILEPPNYGIVTEYASLSGLSDYDINSNRSEEMDMDHMTWAT 112

QY 682 DVAKGMNLYLHRRDP-PIVHRDLKSPNLLVDKYYTVKVCDFGLSRLKARTFLSSKSAAGTP 740

Db 113 DVAKGMNLYLHRRDP-PIVHRDLKSPNLLVDKYYTVKVCDFGLSRLKARTFLSSKSAAGTP 740

QY 741 EWMAPVLRDEPSNEKSDVYSGVILWELATLQOPWCNLPNPAQVAAVGFKGKRLDIPRD 800

Db 171 PMAPEVIQSLPVSETCDTYSYGVVLWEMLTREVPPFKGLEGLQVAVLVVEKNERLTIPSS 230

QY 801 VNPKLASLIVACWADEPWKRPSFSSIMETLKPM 834

Db 231 CPRSFAELLHQWEADAKKRPSFKQIISILESMS 264

RESULT 15

US-09-163-115-5

; Sequence 5, Application US/09163115A

; Patent No. 6183962

; GENERAL INFORMATION:

; APPLICANT: Acton, Susan

; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR

; FILE REFERENCE: MNI-050

; CURRENT APPLICATION NUMBER: US/09/163,115A

; CURRENT FILING DATE: 1998-09-29

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; LENGTH: 455

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-163-115-5

Query Match 11.4%; Score 504.5; DB 3; Length 455;

Best Local Similarity 40.9%; Pred. No. 1.2e-36;

Matches 112; Conservative 41; Mismatches 106; Indels 15; Gaps 4;

QY 564 SLGLEDLVIPWTDLDIREKIGAGSFGTVYRGEWHGSD--VAVKILTEQDFHBERVNEFLR 621

Db 3 SLGASFVQIKFDDDLQFFENC GGSGFSGVYRAKWISQDKEVAVKLLKIE-----K 52

QY 622 EVAIMKSLRHPNIVLFMGAVTKPPNLSIVTEYLSRGSYRLHLHKSQVXKIDETRRINMAF 681

Db 53 EAEILSVLSHRNIIQFYGVILEPPNYGIVTEYASLSGLSDYDINSNRSEEMDMDHMTWAT 112

QY 682 DVAKGMNLYLHRRDP-PIVHRDLKSPNLLVDKYYTVKVCDFGLSRLKARTFLSSKSAAGTP 740

Db 113 DVAKGMNLYLHRRDP-PIVHRDLKSPNLLVDKYYTVKVCDFGLSRLKARTFLSSKSAAGTP 740

QY 741 EWMAPVLRDEPSNEKSDVYSGVILWELATLQOPWCNLPNPAQVAAVGFKGKRLDIPRD 800

Db 171 PMAPEVIQSLPVSETCDTYSYGVVLWEMLTREVPPFKGLEGLQVAVLVVEKNERLTIPSS 230

QY 801 VNPKLASLIVACWADEPWKRPSFSSIMETLKPM 834

Db 231 CPRSFAELLHQWEADAKKRPSFKQIISILESMS 264

Search completed: October 23, 2003, 17:26:12

Job time : 24 secs

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OM protein - protein search, using sw model

Run on: October 23, 2003, 17:25:12 ; Search time 38 Seconds
(without alignments)
3745.830 Million cell updates/sec

Title: US-09-904-389-2
Perfect score: 4435
Sequence: 1 MEMPGRRSDYSLLSQIPDEE.....KPMTKQAPPOQSRDTLSVM 850

Scoring table: BLOSUM62
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Published Applications AA:*
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16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1191.5	26.9	263	10	US-09-840-704-5
4	504.5	11.4	349	15	US-10-106-698-6345
5	504.5	11.4	455	9	US-09-757-982-5
6	467.5	10.5	650	12	US-10-440-341-7
7	467.5	10.5	765	12	US-10-376-564-8
8	460	10.4	659	12	US-10-376-564-7
9	457.5	10.3	425	9	US-09-828-313-29
10	457.5	10.3	648	10	US-09-513-145-6
11	457.5	10.3	648	12	US-10-440-341-3
12	457.5	10.3	648	15	US-10-059-585-38
13	456	10.3	271	10	US-09-840-704-6
14	455	10.3	256	12	US-09-976-782-40
15	455	10.3	257	12	US-09-976-782-29

16	453	10.2	1130	12	US-10-171-889-1	Sequence 1, Appli
17	453	10.2	1130	12	US-10-263-480-2	Sequence 2, Appli
18	452	10.2	1130	12	US-10-204-041-4	Sequence 4, Appli
19	448	10.1	394	10	US-09-862-027-19	Sequence 19, Appl
20	444.5	10.0	746	15	US-10-153-668-436	Sequence 436, App
21	444.5	10.0	859	15	US-10-153-668-324	Sequence 324, App
22	444.5	10.0	892	15	US-10-153-668-438	Sequence 438, App
23	444	10.0	1567	12	US-10-312-918-2	Sequence 2, Appli
24	444	10.0	1594	12	US-10-312-918-4	Sequence 4, Appli
25	440	9.9	847	14	US-10-143-133-2	Sequence 2, Appli
26	438	9.9	1036	12	US-10-354-358-24	Sequence 24, Appl
27	438	9.9	1036	14	US-10-014-882-2	Sequence 2, Appli
28	437.5	9.9	257	11	US-09-823-187-46	Sequence 46, Appl
29	436	9.8	252	12	US-09-976-782-41	Sequence 41, Appl
30	436	9.8	254	12	US-09-976-782-30	Sequence 30, Appl
31	433.5	9.8	651	14	US-10-186-399-2	Sequence 2, Appli
32	433	9.8	966	10	US-09-771-161A-197	Sequence 197, App
33	432	9.7	675	9	US-09-977-269-4	Sequence 4, Appli
34	432	9.7	675	10	US-09-977-260-4	Sequence 4, Appli
35	432	9.7	675	11	US-09-977-261-4	Sequence 4, Appli
36	432	9.7	675	12	US-10-021-660-108	Sequence 108, App
37	432	9.7	675	14	US-10-186-399-3	Sequence 3, Appli
38	432	9.7	686	15	US-10-220-801-12	Sequence 12, Appl
39	424	9.6	604	15	US-10-205-342-1	Sequence 1, Appli
40	420	9.5	606	12	US-10-440-341-5	Sequence 5, Appli
41	417	9.4	251	8	US-08-987-689A-32	Sequence 32, Appl
42	417	9.4	251	15	US-10-292-524-32	Sequence 32, Appl
43	413	9.3	537	12	US-09-976-782-85	Sequence 85, Appl
44	408.5	9.2	1036	10	US-09-771-161A-255	Sequence 255, App
45	408.5	9.2	1036	10	US-09-771-161A-256	Sequence 256, App

ALIGNMENTS

RESULT 1

US-09-904-389-2
; Sequence 2, Application US/09904389
; Patent No. US20020129404A1
; GENERAL INFORMATION:
; APPLICANT: Clendennen, Stephanie K.
; APPLICANT: Schuster, Debra K.
; TITLE OF INVENTION: CTR1 HOMOLOGUE FROM MELON
; FILE REFERENCE: 4257-0029.30
; CURRENT APPLICATION NUMBER: US/09/904,389
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 60/218,307
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 850
; TYPE: PRT
; ORGANISM: Cucumis melo
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (154)...(154)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-904-389-2

Query Match	100.0%;	Score 4433;	DB 10;	Length 850;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches	850;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;
QY	1	MEMPGRRSDYSLLSQIPDEEVGTGASTSFYDVAAGGNVTKGRTDRVFDWDGSGDHRINT	60	
Db	1	MEMPGRRSDYSLLSQIPDEEVGTGASTSFYDVAAGGNVTKGRTDRVFDWDGSGDHRINT	60	
QY	61	QAYRIGNLYSWIGLQHRHSSGSSYDDSLSSDYIYPTLSNPANEINALEYILDDDFRYMK	120	
Db	61	QAYRIGNLYSWIGLQHRHSSGSSYDDSLSSDYIYPTLSNPANEINALEYILDDDFRYMK	120	
QY	121	AVSGSGSGKSWAQQTTEESFQLQQPLVLRLLSDXTCADDPNFMNDPIPDEAALRSLISAE	180	

Db 121 AVSGSGSGKSWAQOTTEESFQLOQPLVLRLSSDXTCADDPNFNDPIPDEAALRLSISAE 180
QY 181 AISHRFVWNGCMSYLEKVPDGFYLIHGMDPYVWSLCTNLQEDGRIPSPESLKTVDSSIGS 240
Db 181 AISHRFVWNGCMSYLEKVPDGFYLIHGMDPYVWSLCTNLQEDGRIPSPESLKTVDSSIGS 240
QY 241 SIEVVLIDRHSDASLKLQNRVHNISSSCVTTKEVADHIAKLVNHLGGSVSEGEDDLVS 300
Db 241 SIEVVLIDRHSDASLKLQNRVHNISSSCVTTKEVADHIAKLVNHLGGSVSEGEDDLVS 300
QY 301 AWKECSDDLKECLGSAVPLCSLSVGLCRHALLFKVLADSIDLPCRIAKGCKYCTRDDA 360
Db 301 AWKECSDDLKECLGSAVPLCSLSVGLCRHALLFKVLADSIDLPCRIAKGCKYCTRDDA 360
QY 361 SSCVRFGLDREYLIDLIGRPGCLCQPDSSLNGPSSISISSPLRPRLKPIESTIDFRSL 420
Db 361 SSCVRFGLDREYLIDLIGRPGCLCQPDSSLNGPSSISISSPLRPRLKPIESTIDFRSL 420
QY 421 AKQYFLDSQSLNLFVDEASSGNVWSGKDAFVYQRPPLNRKDVGKTIIVTGDKDRNSQL 480
Db 421 AKQYFLDSQSLNLFVDEASSGNVWSGKDAFVYQRPPLNRKDVGKTIIVTGDKDRNSQL 480
QY 481 LNKAAQLNTQDGKSEQFRSCVASPYSVQSTPFVENVPLSHISHIGSEDSEHLLALSHP 540
Db 481 LNKAAQLNTQDGKSEQFRSCVASPYSVQSTPFVENVPLSHISHIGSEDSEHLLALSHP 540
QY 541 RMDHVNLPFVHGSQILKPKNELSLGLEDLVIPWTDLDLREKIGAGSGFTVYRGEMHGS 600
Db 541 RMDHVNLPFVHGSQILKPKNELSLGLEDLVIPWTDLDLREKIGAGSGFTVYRGEMHGS 600
QY 601 VAVKILTEQDFHPRVNEFLREVAIMKSLRHPNIVLFMGAVTKPPNLSIVTEYLSRGSLY 660
Db 601 VAVKILTEQDFHPRVNEFLREVAIMKSLRHPNIVLFMGAVTKPPNLSIVTEYLSRGSLY 660
QY 661 RLHLKSGVKDIDETRINMAFDVAKGMNYLHRRDPIVHRDLKSPNLLVDKKTIVKVCDF 720
Db 661 RLHLKSGVKDIDETRINMAFDVAKGMNYLHRRDPIVHRDLKSPNLLVDKKTIVKVCDF 720
QY 721 GLSRLKARTFLSSKSAAGTPEWMAPEVLRDEPSNEKSDVYSFGVILWELATLQPPWCNIN 780
Db 721 GLSRLKARTFLSSKSAAGTPEWMAPEVLRDEPSNEKSDVYSFGVILWELATLQPPWCNIN 780
QY 781 PAQVVAAGFKGKRLDIPRDVNPKLASLIVACWADEPWKRPSFSSIMETLKPMTKQAPPQ 840
Db 781 PAQVVAAGFKGKRLDIPRDVNPKLASLIVACWADEPWKRPSFSSIMETLKPMTKQAPPQ 840
QY 841 QSRTDTLSVM 850
Db 841 QSRTDTLSVM 850

RESULT 2
US-10-171-404A-48
; Sequence 48, Application US/10171404A
; Publication No. US20030177529A1
; GENERAL INFORMATION:
; APPLICANT: BASF PLANT SCIENCE GMBH
; TITLE OF INVENTION: SUGAR AND LIPID METABOLISM REGULATORS IN PLANTS II
; FILE REFERENCE: 16313-0119
; CURRENT APPLICATION NUMBER: US/10/171,404A
; PRIOR FILING DATE: 2002-11-19
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 821
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-171-404A-48

Query Match 61.8%; Score 2742.5; DB 12; Length 821;

Best Local Similarity 62.3%; Pred. No. 1.6e-219;
Matches 546; Conservative 99; Mismatches 144; Indels 87; Gaps 14;
QY 1 MEMPGRRSDYSLLSQIPDEEVG---TCGSTSFYDSVAA-----GGNVIKGRTDR-VFD 49
Db 1 MEMPGRRSNYTLLSQFSDDDQSVSVTGAPPHYDLSLSSENRSNHNNGTGTAKAERGSGFD 60
QY 50 WD----GSGDHRINTQAYRIG-NLY-SWICLQRHSSGSSYDDSSLSDDYYAPTLSNPAAN 103
Db 61 WDPGSGGGGDHRLNPNRVGNMYASSLGLQRQSSGSSFGESSISGDYYMPTLS-AAAN 119
QY 104 EINALLEYILDDDFRV-----MKAVGSGG-SSGKSWAQOTTEESFQLOQPLVLRL 150
Db 120 EIESVGFPQDDGFRLCFGGGGDLRIQMAADSAGSSSGKSWAQOTTEESYQLQALALRL 179
QY 151 SSDXTCADDPNFMDDPIDEAALRLSLSISAEASHRFWNGCMSYLEKVPDGFYLIHGMDP 210
Db 180 SSEATCADDPNFLDPVDESAIRTSPPSSAETVSHRFWNGCLSYVDKVPDGFYMMNGLDP 239
QY 211 YVWSLCTNLQEDGRIPSPESLKTVDSSIGSSIEVVLIDRHSDASLKLQNRVHNISSSCV 270
Db 240 YIWTLCIDLHESGRIPSPESLRAVDSGVDSLSLEAIIVDRRSDPAFKELHNRVHDISCS 299
QY 271 TTKEVADHIAKLVNHLGGSVSEGEDDLVSAWKECSDDLKECLGSAVPLCSLSVGLCRH 330
Db 300 TTKEVVDQALAKLICNRMGPGVIMGEDELVPMWKECIDGLKE-IFKVVPVIGSLVGLCRH 358
QY 331 RALLFKVLADSIDLPCRIAKGCKYCTRDDASSCLVRFGLDREYLIDLIGRPGCLCQPD 390
Db 359 RALLFKVLADIIDLPCRIAKGCKYCNRDDAASCLVRFGLDREYLVDLVGKPGHLWEF 418
QY 391 LNPSSSISISSPLRFPRLKPIESTIDFRSLAKQYFLDSQSLNLFVDEASSGNVSGKDA 450
Db 419 LNPSSSISISSPLRFPRLKPIESTIDFRSLAKQYFSDSQSLNLFVDEPASD-----DMG 471
QY 451 FSVYQRPPLNRKDVGKTIIVTGDKDRNSQLLNKAAQLNTQDGKSEQFRSCVASPYSVQ 510
Db 472 FSMFHRQYDNPGGENDALAENG-----QNMVRASNQIEAAPMNPPIQPVNRA 544
QY 511 TPFEVNVVPLSHISHIGSEDSEHLLALSHPRMDHVNLPFVHGSQILKPKNELSLGLE 570
Db 497 LPPSANMPP-----QNMVRASNQIEAAPMNPPIQPVNRA 544
QY 571 VIPWTDLDLREKIGAGSGFTVYRGEMHGSVAVKILTEQDFHPRVNEFLREVAIMKSLR 630
Db 545 DIPWCDLNIKEKIGAGSGFTVHRAEWHGSDVAVKILMEQDFHAERVNEFLREVAIMKRLR 604
QY 631 HPNIVLFWGAVTKPPNLSIVTEYLSRGSLYRLHLKSGVKD-IDETRINMAFDVAKGMNY 689
Db 605 HPNIVLFWGAVTQPPNLSIVTEYLSRGSLYRLHLKSGAREQLDERRLSKSAAGTPEWMAPEVLR 749
QY 690 LHRRDPPPIVHRDLKSPNLLVDKKTIVKVCDFGLSRLKARTFLSSKSAAGTPEWMAPEVLR 724
Db 665 LHNRNPPPIVHRDLKSPNLLVDKKTIVKVCDFGLSRLKARTFLSSKSAAGTPEWMAPEVLR 724
QY 750 DEPSNEKSDVYSFGVILWELATLQPPWCNINPAQVVAAGFKGKRLDIPRDVNPKLASLI 809
Db 725 DEPSNEKSDVYSFGVILWELATLQPPWCNINPAQVVAAGFKGKRLDIPRDVNPQVAAII 784
QY 810 VACWADEPWKRPSFSSIMETLKPMTKQAPPQSRD 845
Db 785 EGCWTNEPWKRPSFATIMDLRLPLIKSAVPPPPNRSD 820

RESULT 3
US-09-840-704-5
; Sequence 5, Application US/09840704
; Patent No. US20020122801A1
; GENERAL INFORMATION:
; APPLICANT: Dedhar, Shoukat
; APPLICANT: Hannigan, Greg
; TITLE OF INVENTION: Intergrin-Linked Kinase and its Uses
; FILE REFERENCE: KIN-2CON

; CURRENT APPLICATION NUMBER: US/09/840,704
; CURRENT FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/566,906
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US08/752,345
; PRIOR FILING DATE: 1996-11-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 263
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (1)...(263)
US-09-840-704-5

Query Match 26.9%; Score 1191.5; DB 10; Length 263;
Best Local Similarity 84.4%; Pred. No. 5.6e-91;
Matches 222; Conservative 25; Mismatches 15; Indels 1; Gaps 1;

QY 572 IPWTDLDLREKIGAGSFGTVYRGEGHGSVAVKILTEQDFHPERVNEFLREVAIMKSLRH 631
Db 1 IPWCDLNIKEKIGAGSFGTVHRAEWHGSDVAVKILMEQDFHAEVNEFLREVAIMKSLRH 60

QY 632 PNIIVFMGAVTKPPNLSIVTEYLSRGLYRLHKGSKVD-IDETRRINMAFDVAKGMNYL 690
Db 61 PNIIVFMGAVTQPPNLSIVTEYLSRGLYRLHKGSGAREQDERRRLSMAYDVAKGMNYL 120

QY 691 HRRDPPVHRDLKSPNLLVDKKTYYKVCDFGLSRLKARTFLSSKSAAGTPWMAPEVLRD 750
Db 121 HNRNPPVHRDLKSPNLLVDKKTYYKVCDFGLSRLKASTFLSSKSAAGTPWMAPEVLRD 180

QY 751 EPSNEKSDVYSFGVILWELATLQOPWCNLPNAQVVAAGVFGKGRKLDIPRDVNPKLASLIV 810
Db 181 EPSNEKSDVYSFGVILWELATLQOPWCNLPNAQVVAAGVFGKGRKLEIPRNLNPQVAAIE 240

QY 811 ACWADEPWKRPSFSSIMETLKPM 833
Db 241 GCWTNEPWKRPSFATIMDLLRPL 263

RESULT 4
US-10-106-698-6345
; Sequence 6345, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005PI
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 6345
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (340)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-6345

Query Match 11.4%; Score 504.5; DB 15; Length 349;
Best Local Similarity 40.9%; Pred. No. 1.6e-33;
Matches 112; Conservative 41; Mismatches 106; Indels 15; Gaps 4;

QY 564 SIGLEDLVIPWTDLDLREKIGAGSFGTVYRGEGHGS--VAVKILTEQDFHPERVNEFLR 621
Db 59 SLGASFVQIKFDDLOFFENCNGGSGFSGVYRAKWISQDKEVAVKLLKIE-----K 108

QY 622 EVAIMKSLRHPNIVLFMGAVTKPPNLSIVTEYLSRGLYRLHKGSKVDIDETRRINMAF 681
Db 109 EAEILSVLSHRNIIQFYGVILEPPNYGIVTEYASLGLSYDYINSNRSEEMDMDHIMTWAT 168

QY 682 DVAKGMNYLHRRDP-PIVHRDLKSPNLLVDKKTYYKVCDFGLSRLKARTFLSSKSAAGTP 740
Db 169 DVAKGMHYLHMEAPVKVIHRDLKSRNVVIAADGVLKICDFGASRFNHT--THMSLVGTF 226

QY 741 EWMAPEVLRDEPSNEKSDVYSFGVILWELATLQOPWCNLPNAQVVAAGVFGKGRKLDIPRD 800
Db 227 PWMAPEVIQSLPVSETCDTYSYGVVLWEMLTREVPPFKGLEGLQVAVLWVEKNERLTIPSS 286

QY 801 VNPKLASLIVACWADEPWKRPSFSSIMETLKPM 834
Db 287 CPRSFAELLHQCWEADAKKRPSFKQIISILESMS 320

RESULT 5
US-09-757-982-5
; Sequence 5, Application US/09757982
; Patent No. US20020094559A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCES: MNI-050
; CURRENT APPLICATION NUMBER: US/09/757,982
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 09/163,115
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-757-982-5

Query Match 11.4%; Score 504.5; DB 9; Length 455;
Best Local Similarity 40.9%; Pred. No. 2.4e-33;
Matches 112; Conservative 41; Mismatches 106; Indels 15; Gaps 4;

QY 564 SIGLEDLVIPWTDLDLREKIGAGSFGTVYRGEGHGS--VAVKILTEQDFHPERVNEFLR 621
Db 3 SLGASFVQIKFDDLOFFENCNGGSGFSGVYRAKWISQDKEVAVKLLKIE-----K 52

QY 622 EVAIMKSLRHPNIVLFMGAVTKPPNLSIVTEYLSRGLYRLHKGSKVDIDETRRINMAF 681
Db 53 EAEILSVLSHRNIIQFYGVILEPPNYGIVTEYASLGLSYDYINSNRSEEMDMDHIMTWAT 112

QY 682 DVAKGMNYLHRRDP-PIVHRDLKSPNLLVDKKTYYKVCDFGLSRLKARTFLSSKSAAGTP 740
Db 113 DVAKGMHYLHMEAPVKVIHRDLKSRNVVIAADGVLKICDFGASRFNHT--THMSLVGTF 170

QY 741 EWMAPEVLRDEPSNEKSDVYSFGVILWELATLQOPWCNLPNAQVVAAGVFGKGRKLDIPRD 800
Db 171 PWMAPEVIQSLPVSETCDTYSYGVVLWEMLTREVPPFKGLEGLQVAVLWVEKNERLTIPSS 230

QY 801 VNPKLASLIVACWADEPWKRPSFSSIMETLKPM 834
Db 231 CPRSFAELLHQCWEADAKKRPSFKQIISILESMS 264

RESULT 6
US-10-440-341-7
; Sequence 7, Application US/10440341
; Publication No. US20030181413A1
; GENERAL INFORMATION:
; APPLICANT: RAPP, ULF

APP, HARALD
STORM, STEPHEN M.
TITLE OF INVENTION: RAF PROTEIN KINASE THERAPEUTICS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVE., N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/440,341
FILING DATE: 15-May-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/748,931
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 5683/82731
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 650 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-440-341-7

QY 808 LIVACWADEPWKRPSFSSIMETLKPMTKQAP 838
Db 576 LMAECLKKRRDERPLFPQILASIELLARSIP 606
RESULT 7
US-10-376-564-8
; Sequence 8, Application US/10376564
; Publication No. US20030180302A1
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckhard
; APPLICANT: Werner, Sabine
; APPLICANT: Halle, Jörn-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
; TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
; TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
; TITLE OF INVENTION: Active Substances
; FILE REFERENCE: 50125/014003
; CURRENT APPLICATION NUMBER: US/10/376,564
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 09/886,319
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/222,081
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: DE 100 30 149.5-41
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-376-564-8
Query Match 10.5%; Score 467.5; DB 12; Length 765;
Best Local Similarity 31.0%; Pred. No. 6.3e-30;
Matches 140; Conservative 80; Mismatches 166; Indels 65; Gaps 17;
QY 419 SLAKQYFLDSQSLNLFVDEASSGNVVGKDAAFSV-YQRPLNRKDVGDKTIVVTGDKORN 477
Db 305 SLAETALTSGSSPSAPASDSIGPQLTSPSPKSIPIQPFRPADEHNRN--QFGQRDRS 362
QY 478 SQLLNKAAQLNTQDG-----KSEQFRSCVASPYSVQSTP-----FVENVVEL----- 520
Db 363 SSAPN---VHINTIEPVNIDDLIRDOGFRGGSTTGLSATPPASLPGLSLTNVKALQKSP 419
QY 521 ----SHISHIGSEDSEHLLALSHPRMDHVNLPFVHGSQQLIRKPNELSLGLEDLVIPWTD 576
Db 420 GPQERKSSSSSEDRNRMKTIG--RRD-----SSDDWEIPDGQ 455
QY 577 LDLREKIGAGSFGTVYRGEGWHSADVAVKILTEQDFHPERVNEFLREVAIMKSLRHPNIVL 636
Db 456 ITVGQRIGSGSFGTVYKGKWHG-DVAVKMLNVTAPTQQLOAFKNEVGVLKTRHVNILL 514
QY 637 FMGAVTKPPNLSIVTVEYLSRGSlyRLHLKSGVKDIDETRRINNAFDVAKGMNYLHRDPP 696
Db 515 FMGYSTK-PQLAIVTQWCEGSSLYHLLHIETK-FEMIKLIDIAARQTAQGM DYLHAKS-- 570
QY 697 IVHRDLKSPNLLVDKKYTVKVCDFGLSRLKARTFLSS--KSAAGTPEWMAPEVLRDPSN 754
Db 571 ITHRDLKSNIFLHEDLTVKIGDFGLATVKSRWSGSHQFEQLSGSILWMAPEVIRMQDKN 630
QY 755 E---KSDVYSFGVILWELATLQQPWCNLPNPA-QVVAAV--GFKGKRLDIPRDVNPX-LAS 807
Db 631 PYSFQSDVYAFGIVLYELMTGQLPYSNINNRDQIIFMVGRGYLSPDLSKVRSNCPKAMKR 690
QY 808 LIVACWADEPWKRPSFSSIMETLKPMTKQAP 838
Db 691 LMAECLKKRRDERPLFPQILASIELLARSIP 721

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RESULT 8
US-10-376-564-7
; Sequence 7, Application US/10376564
; Publication No. US20030180302A1
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckhard
; APPLICANT: Werner, Sabine
; APPLICANT: Halle, Jorn-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
; TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
; TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
; TITLE OF INVENTION: Active Substances
; FILE REFERENCE: 50125/014003
; CURRENT APPLICATION NUMBER: US/10/376,564
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 09/886,319
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/222,081
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: DE 100 30 149.5-41
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-376-564-7

Query Match      10.4%; Score 460; DB 12; Length 659;
Best Local Similarity 39.3%; Pred. No. 2.1e-29;
Matches 110; Conservative 59; Mismatches 97; Indels 14; Gaps 9;

QY 568 EDLVIPWTDLDLREKIGAGSFGTVYRGWGHGSDVAVKILTEQDFHPERVNEFLREVAIMK 627
Db 341 DDWEIPDGOITVQGRIGSGSFGTVYRGKWHG-DVAVKMLNVTAFTPTQQLQAFKNEVGVL 399

QY 628 SLRHPNIVLFMGAVTKPPNLSIVTEYLSRGSLYRLHLKSGVKDIDETRRINMAFDVAKGM 687
Db 400 KTRHVNILFMGYSTK-PQLAIVTQWCEGSSLYHHLHIETK-FEMIKLIDARQTAQGM 457

QY 688 NYLHRRDPPIVHRDLKSPNLLVDKKTVCDFGLSRKARTFLSS--KSAAGTPEWMA 745
Db 458 DYLAHKS--IHRDLKSNIFLHEDITVKIGDFGLATVKSRWSGSHQFQLSGSILWMA 515

QY 746 EVLRDEPSNE---KSDVYSGVILWELATLQOPWCNLPNPA-QVVAAV--GFKGKRLDIPR 799
Db 516 EVIRMQDNKPNYSFQSDVYAFGIVLYELMTGQLPYSNINRPDQIIFMVGRGYSPLSKVR 575

QY 800 DVNPK-LASLIVACWADEPWKRPSFSIMETLKPMTKQAP 838
Db 576 SNCPKAMRLMABCLKKRDERPLFPQILASIALLARSLP 615

RESULT 9
US-09-828-313-29
; Sequence 29, Application US/09828313
; Patent No. US20020059662A1
; GENERAL INFORMATION:
; APPLICANT: COSTA e SILVA, OSWALDO DA
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: THIELEN, NOCHA VAN
; APPLICANT: CHEN, ROUYING
; APPLICANT: SARRIA-MILLAN, RODRIGO
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
; TITLE OF INVENTION: USE IN PLANTS
; FILE REFERENCE: 16313-0032
; CURRENT APPLICATION NUMBER: US/09/828,313
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
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; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Physcomitrella patens
US-09-828-313-29

Query Match      10.3%; Score 457.5; DB 9; Length 425;
Best Local Similarity 31.3%; Pred. No. 1.8e-29;
Matches 128; Conservative 73; Mismatches 139; Indels 69; Gaps 14;

QY 456 RPLNRKDVDCGTIIVTGDKDRNSQL-----LNKAAQLNTQD--GKSEQFR 499
Db 27 RTILKCD--KQLVNAADYDKRTPHLIAASLDCVPVAKVLLAEGAELNAKDRWGSPPRGE 83

QY 500 SCVASPYSVQSTPFVENVVPLSHI---SHIGSEDSEHLLALSHPRMDHVNNL-----PFV 551
Db 84 A-----ESAGYMEMVKLLKDYGAESHAGA-----PR-GHVESLIQVAPPLP 123

QY 552 HGSQQLIRKPNELSLGLEDLVIPWTDLDLREKIGAGSFGTVYRGWGHGSDVAVKILTEQDF 611
Db 124 SNRDWEIAPSEI-----ELDTSELIGKGAFGIRKALWRGTPVAVKTI-RPSL 170

QY 612 HPER--VNEFLREVAIMKSLRHPNIVLFMGAVTKPPNLSIVTEYLSRGSLYRLHLKSGVK 669
Db 171 SNDRMVIKDFQHEVQLLVKVRHPNIVQFLGAVTRQRPMLVTEFLAGGDLHQLLRSN--P 228

QY 670 DIDETRRINMAFDVAKGMNYLHRRDPPIVHRDLKSPNLLVDKKTVCDFGLSRL----- 725
Db 229 NLAPDRIVKYALDIARGMSYLNRSKPIIHRDLKPRNIIVDEEHELKVGDFGLSKLIDVK 288

QY 726 KARTFLSSKSAAGTPEWMAPEVLRDEPSNEKSDVYSGVILWELATLQOPWCNLPNPAQW 785
Db 289 LMHDVYKMTGSGSYRYMAPEVFEHQPYDKSDVDFSGMILYEMFEGVAPFEDKDAYDAA 348

QY 786 AAVGFKGKRLDI-PRDVNPKLASLIVACWADEPWKRPSFSIMETLKP 833
Db 349 TLVARDDKRPEMRAQTYPPQMKALIEDCWSPTYTPKRPPFVEIVKKLEVM 397

RESULT 10
US-09-513-145-6
; Sequence 6, Application US/09513145
; Publication No. US20020192723A1
; GENERAL INFORMATION:
; APPLICANT: Yoo, Tai-June
; TITLE OF INVENTION: Antigen to Systemic Lupus Erythematosis and Diagnostic
; TITLE OF INVENTION: Assay
; FILE REFERENCE: 2502-1-2
; CURRENT APPLICATION NUMBER: US/09/513,145
; CURRENT FILING DATE: 2000-02-25
; EARLIER APPLICATION NUMBER: 60/121548
; EARLIER FILING DATE: 1999-02-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-145-6

Query Match      10.3%; Score 457.5; DB 10; Length 648;
Best Local Similarity 35.3%; Pred. No. 3.3e-29;
Matches 125; Conservative 68; Mismatches 116; Indels 45; Gaps 14;

QY 503 ASPYSVQSTPFVENVVPLSHISHIGSEDSEHLLALSHPRMDHVNLPFVHGSQILRKENE 562
Db 288 ASPSALSSSP-----NNLSPTGWSQKTPVPAQRERAP-----VSGTQ--EKNKI 330

QY 563 LSUGLEDLVIPW----TDLDLREKIGAGSFGTVYRGWGHGSDVAVKILTEQDFHPERVNE 618
Db 331 RPRQRDSSYYWEIEASEVMLSTRIGSGSGTVYKGKWHG-DVAVKILKVVDPPTPEQFOA 389
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QY 619 FLREVAIMKSLRHPNIVLFMGAVTKPPNLSIVTEYLSRGSlyRLLLHKSGVKDIDETR--- 675
Db 390 FRNEVAVLRKTRHVNILLFMGYMTK-DNLAIVTQWCEGSSLYKHLH-----VQETKFQM 442
QY 676 --RINMAFDVAKGMNLYLHRRDPPPIVHRDLKSPNLLVDKKYTVKVCDFGLSRLKARTFLSS 733
Db 443 FQLIDIAARQTAQGMNDYLHAKN--IIHRDMKSNIFLHHEGLTVKIGDFGLATVKSRWSGSQ 500
QY 734 --KSAAGTPENMAPEVLR---DEPSNEKSDVYSFGVILWELATLQOPWCNLPNPA-QVVAA 787
Db 501 QVEQPTGSLVWMAPEVIRMQDNNPFSQSDVYSYGIVLYELMTGELPYSHINNRDQIIFM 560
QY 788 VGFKGKRLDIPRDVN--PKLASLIVA-CWADEPWKRPSFSSIMETLKPMTKQAP 838
Db 561 VGRGYASPDLSKLYKNCPCPKAMKRLVADCVKKVKEERPLFPQILSSIELLOHSLP 614

RESULT 11
US-10-440-341-3
; Sequence 3, Application US/10440341
; Publication No. US20030181413A1
; GENERAL INFORMATION:
; APPLICANT: RAPP, ULF
; APP, HARALD
; STORM, STEPHEN M.
; TITLE OF INVENTION: RAF PROTEIN KINASE THERAPEUTICS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVE., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/440,341
; FILING DATE: 15-May-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/748,931
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: 5683/82731
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3067
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-440-341-3

Query Match 10.3%; Score 457.5; DB 12; Length 648;
Best Local Similarity 35.3%; Pred. No. 3.3e-29;
Matches 125; Conservative 68; Mismatches 116; Indels 45; Gaps 14;
QY 503 ASPYSVQSTPFVENVVLPSLHSHIGSEDEHLLALSHPRMDHVNLLPFVHGSQILRKPNE 562
Db 288 ASPSALSSSP-----NNLSPTGWSQKTPVPAQRERAP-----VSGTQ--EKWKI 330

QY 563 LSLGLEDLVIPW----TDLDREKIGAGSFGTVYRGWHGSDVAVKILTEQDFHPERVNE 618
Db 331 RPRGORDSSYYWEIEASEVMLSTRIGSGSFGTVYKGKWHG-DVAVKILKVVDPTEQFQA 389
QY 619 FLREVAIMKSLRHPNIVLFMGAVTKPPNLSIVTEYLSRGSlyRLLLHKSGVKDIDETR--- 675
Db 390 FRNEVAVLRKTRHVNILLFMGYMTK-DNLAIVTQWCEGSSLYKHLH-----VQETKFQM 442
QY 676 --RINMAFDVAKGMNLYLHRRDPPPIVHRDLKSPNLLVDKKYTVKVCDFGLSRLKARTFLSS 733
Db 443 FQLIDIAARQTAQGMNDYLHAKN--IIHRDMKSNIFLHHEGLTVKIGDFGLATVKSRWSGSQ 500
QY 734 --KSAAGTPENMAPEVLR---DEPSNEKSDVYSFGVILWELATLQOPWCNLPNPA-QVVAA 787
Db 501 QVEQPTGSLVWMAPEVIRMQDNNPFSQSDVYSYGIVLYELMTGELPYSHINNRDQIIFM 560
QY 788 VGFKGKRLDIPRDVN--PKLASLIVA-CWADEPWKRPSFSSIMETLKPMTKQAP 838
Db 561 VGRGYASPDLSKLYKNCPCPKAMKRLVADCVKKVKEERPLFPQILSSIELLOHSLP 614

RESULT 12
US-10-059-585-38
; Sequence 38, Application US/10059585
; Publication No. US20030082776A1
; GENERAL INFORMATION:
; APPLICANT: Ota, Toshio
; APPLICANT: Isogai, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Hayashi, Koji
; APPLICANT: Otsuka, Kaoru
; APPLICANT: Yamamoto, Jun-ichi
; APPLICANT: Ishii, Shizuko
; APPLICANT: Sugiyama, Tomoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Keiichi
; APPLICANT: Otsuki, Tetsuji
; APPLICANT: Funahashi, Shin-Ichi
; APPLICANT: Senoo, Chiaki
; APPLICANT: Nezu, Jun-Ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
; TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
; FILE REFERENCE: 06501-098001
; CURRENT APPLICATION NUMBER: US/10/059,585
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05060
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-059-585-38

Query Match 10.3%; Score 457.5; DB 15; Length 648;
Best Local Similarity 35.3%; Pred. No. 3.3e-29;
Matches 125; Conservative 68; Mismatches 116; Indels 45; Gaps 14;
QY 503 ASPYSVQSTPFVENVVLPSLHSHIGSEDEHLLALSHPRMDHVNLLPFVHGSQILRKPNE 562
Db 288 ASPSALSSSP-----NNLSPTGWSQKTPVPAQRERAP-----VSGTQ--EKWKI 330

563	QY	LSLGLD	LVIPW----	TDL	DLREKIGAGSFGTVYRG	EHGSDVAVKILTEQDFH	PERVNE	618	
331	Db	RPRGQR	DSSYYWEI	EASEV	MLSTRIGSGF	GVYKWKHG-DVAVKIL	KWVDP	TPPEQFOA 389	
619	QY	FLREVA	IMKSLRHP	NI	VLFWGAVTKPP	NLSIVTEYLSRGS	LYRL	LHKSGVKDIDETR--- 675	
390	Db	FRNEVA	VLKTRHVN	ILLFWGY	MTK-DNLAIVTQ	CEGSSLYKHLH-----	VQETK	FQM 442	
676	QY	--RINMA	FDVAKGM	NYLHR	DPPIVHRDLK	SPNLLVDK	YTVK	VCDFGLSRLKARTFLSS 733	
443	Db	FQLIDIA	RQTAQGM	DYLHAKN--	IHRDMKSN	NI	FLHEGLTVKIGD	FGLATVKS	RWSGSQ 500
734	QY	--KSAAG	TPENMAPE	VL---	DEPSNEKSD	VYSFGVILWELATL	QQPWC	NLNP	A-QVVA 787
501	Db	QVEQPT	GSVLWMAPE	IRMQD	NNPFSFQSD	VYSYGIVLYEL	MTGELPYSH	INNRDQIIFM 560	
788	QY	VGPKG	KRLDIP	RDVN--	PKLAS	LIVA-CWADEP	WKRPSP	FSSIMETL	KPMTKOAP 838
561	Db	VGRG	VASPDLSK	LYKNCP	PRAMKRLVAD	CVKKVKEERL	FPQILSS	IELH	OSLP 614

RESULT 13

```

US-09-840-704-5
; Sequence 6, Application US/09840704
; Patent No. US20020122801A1
; GENERAL INFORMATION:
; APPLICANT: Dedhar, Shoukat
; APPLICANT: Hannigan, Greg
; TITLE OF INVENTION: Intergrin-Linked Kinase
; FILE REFERENCE: KIN-2CON
; CURRENT APPLICATION NUMBER: US/09/840,704
; CURRENT FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/566,906
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US08/752,345
; PRIOR FILING DATE: 1996-11-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 271
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (1)...(271)
;
US-09-840-704-6

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[illegible]

RESULT 14

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US-09-976-782-40
; Sequence 40, Application US/09976782
; Publication No. US20030190715A1
; GENERAL INFORMATION:
;   APPLICANT: Grosse et al
;   TITLE OF INVENTION: No. US20030190715A1e1
;   FILE REFERENCE: 21402-157
;   CURRENT APPLICATION NUMBER: US/09/976,782
;   CURRENT FILING DATE: 2001-10-12
;   PRIOR APPLICATION NUMBER: 60/240,113
;   PRIOR FILING DATE: 2000-10-12
;   PRIOR APPLICATION NUMBER: 60/240,662
;   PRIOR FILING DATE: 2000-10-16
;   PRIOR APPLICATION NUMBER: 60/240,732
;   PRIOR FILING DATE: 2000-10-16
;   PRIOR APPLICATION NUMBER: 60/240,625
;   PRIOR FILING DATE: 2000-10-16
;   PRIOR APPLICATION NUMBER: 60/240,703
;   PRIOR FILING DATE: 2000-10-16
;   PRIOR APPLICATION NUMBER: 60/241,190
;   PRIOR FILING DATE: 2000-10-16
;   PRIOR APPLICATION NUMBER: 60/240,637
;   PRIOR FILING DATE: 2000-10-16
;   PRIOR APPLICATION NUMBER: 60/240,669
;   PRIOR FILING DATE: 2000-10-16
;   PRIOR APPLICATION NUMBER: 60/262,455
;   PRIOR FILING DATE: 2001-01-18
;   PRIOR APPLICATION NUMBER: 60/240,648
;   PRIOR FILING DATE: 2000-10-16
;   NUMBER OF SEQ ID NOS: 127
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial
;   OTHER INFORMATION: sequence
US-09-976-782-40

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Query Match	10.3%;	Score 455;	DB 12;	Length 256;
Best Local Similarity	40.0%;	Pred. No. 1.3e-29;		
Matches 104;	Conservative 50;	Mismatches 94;	Indels 12;	Gaps 7;

QY	579	LREKIGAGSFGTYRGGEWHGS-----DVAVKILTEQDFHPRVNEFLREVAIMKSLRHPN	633
Db	1	LGKKLGEAGFGEVYGTLLKGKGVEVEAVKTLKE-DASEQQIEEFLREARLMRKLDPN	59
QY	634	IVLFMGAVTKPPNLSIVTEYLSRGLYRLLHKSGVKDIDETRRINMAFDVAKGMNYLHRR	693
Db	60	IVKLLGVCTEEEEPLMIVMEYMEGGDLLDYLRKNRPKELSLSDLLSPALQIARGMEYLESK	119
QY	694	DEPIVHRDLKSPNLLVDKKYTVKVCDFGLSR-LKARTFLSSKSAAGTP-EWMAPEVLRDE	751
Db	120	N--FVHRDLAARNCLVGENKTVKIADFGIARDLYDDDYRKKKSPRLPIRWMAPESLKOG	177
QY	752	PSNEKSDVYSFGVILWELATL-QQPWCNLPAAQVAAVGFKGKRLDIPRDVNPKLASLIV	810
Db	178	KFTSKSDVWSFGVLLWEIFTLGESPYPGMSNEEVLEYLK-KGYRLFPQPNCPDEIYDML	236
QY	811	ACWADEPWKRPSFSSIMETL	830
Db	237	OCWAEDPEDRPTFSELVERL	256

RESULT 15

US-09-976-782-29
; sequence 29, Application US/09976782
; Publication No. US20030190715A1
; GENERAL INFORMATION:
; APPLICANT: Grosse et al
; TITLE OF INVENTION: No. US200301907
; FILE REFERENCE: 21402-157

Sat Oct 25 11:01:51 2003

; CURRENT APPLICATION NUMBER: US/09/976,782
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,113
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,662
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,732
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,625
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,703
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/241,190
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,637
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,669
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/262,455
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/240,648
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Consensus
; OTHER INFORMATION: sequence
;
US-09-976-782-29

Query Match 10.3%; Score 455; DB 12; Length 257;
Best Local Similarity 40.0%; Pred. No. 1.3e-29;
Matches 104; Conservative 50; Mismatches 94; Indels 12; Gaps 7;

QY 579 LREKIGAGSGFTVYRGEWHGS-----DVAVKILTEQDHPHPRVNEFLREVAIMKSLRHPN 633
Db 2 LGKLGEGAFGEVYKGTLLKGGVGEVAVKTLKE-DASEQQIEEFLREARLKRKLDHPN 60

QY 634 IVLFMGAVTKPPNLSIVTEYLSRGSYLRLHLHKSGVKDIDETRRINMAFDVAKGMNYLHRR 693
Db 61 IVKLLGVCTEEEPIMIVMEYMEGGDLDLYLRKNRPKELSLSDLLSFALQIARGWEYLESK 120

QY 694 DPPIVHRDLKSNLLVDKCYTVKVCDFGLSR-LKARTFLSSKSAAGTP-ENWAPPEVLRDE 751
Db 121 N--FVHRDLAARNCLVGENKTVKIADFGIARDLYDDDYRKKKSPRLPIRMWAPESLKDQ 178

QY 752 PSNEKSDVYSFGVILWELATL-QQPCWNLNPAQVAAVGFKGKRLDIPROVNPKLASLIV 810
Db 179 KPTSKSDVWSFGVLLWEIFTLGESPYPGNSNEEVLEYLK-KGYRLPQPPNCPDEIYDLML 237

QY 811 ACWADEPWKRPSFSIMETL 830
Db 238 QCWAEDPEDRPTFSELVERL 257

Search completed: October 23, 2003, 17:30:39
Job time : 42 secs

QY 1348 CCAAGACTAAACCTATTGAATCTACCATTTGATTTTCTAGGTCACCTGGCCAAACAGTATTC 1407
Db 1417 CCACGACCAAGGCCAGTTGAACCCGCGAGTCGATTTTAGGTTACTAGCCAAACAATATTC 1476
QY 1408 TTGGATAGCCCAATCATTAACTTTGATTTTATGATGAAGCTTCTTCAGGTAATGTTGTATCT 1467
Db 1477 TCCGATAGCCAGTCTCTTAATCTTGTCTTCGATCCTGCATCAG----- 1519
QY 1468 GGGGAAGGATGCTGCATCTTCCTGCTATCAAGGCCATTAAATAGGAAGGATGTAGATGGA 1527
Db 1520 ----ATGATATGGGATTTCTCAATGTTTTCATAGGCAATATGATAATCCGGTGGAGAGAT 1575
QY 1528 AAAACCATAGTGGTTACTGGTGACAAGGACAGAAATTTCTCAGTTATTAATAAAAAAGCA 1587
Db 1576 GACGCATTGGCAGAAAATGGTG----- 1597
QY 1588 GCCCAACTGAATACTCAAGATGGAAAGTCTGAGCAATTTAGATCATGTGTGTTCTCTCCA 1647
Db 1598 ----- 1597
QY 1648 TATAGTGTACAGTCGACCCCTTTTGTAGAAAATGTAGTCCCTTTTAAGCCATATCTCACAC 1707
Db 1598 -----GTGGTCTTTGCCACCC 1614
QY 1708 ATTGTTCTGAAGATTCGGAGCATCTCTTAGCAATGTCTCATCCAAGGATGGATCATGTT 1767
Db 1615 AGTGCTAATATGCTTCCACAGAACATGATGCGTGCGTCAAAATCAAAATGAAGCAGCACCT 1674
QY 1768 AACAAATTTACCAATTTGTTTCATGCTAGTCAAGTTGATAGAAAACCAATAGACTTTTCCCTT 1827
Db 1675 ATGAATGCCCCACCAATCAGTCAGCCAGTTTCCAAACAGGGCAAAATAGGGAACCTTGACCTT 1734
QY 1828 GGCTTAGAAGATTTGGTTATTCATGGACAGATCTTCAATTTGAGGGAGAAAATTTGGAGCA 1887
Db 1735 GATGGTGATGATATGGACATCCCGTGGTGTGATCTTAATATAAAAGAAAGATTGGAGCA 1794
QY 1888 GGTCTCTTTGGGACTGTATATCGTGGTGAGTGGCATGCTCTGATGTTGCTGTGAAGATC 1947
Db 1795 GGTTCCTTTGGCACTGTCCACCGTCTGAGTGGCATGCTCGGATGTTGCTGTGAAAATT 1854
QY 1948 CTCACAGAACAGACTTCCATCCTGAACGTGTTAAATGAGTTTCTGAGAGAGTTGCTATC 2007
Db 1855 CTCATGGAGCAAGACTTCCATGCTGAGCGTGTAAATGAGTTCTTAAGAGAGGTTGGGATA 1914
QY 2008 ATGAAATCTTTACGACATCCTAATATTTACTGTTTATGGGTGCGGTGACCAAGCCACCA 2067
Db 1915 ATGAAACGCTTCGCCACCCCTAACATTTCTCTTCATGGGTGCGGTCACTCAACCTCCA 1974
QY 2068 AACTTGTCCATTGTCACCGAATATCTATCGAGAGGTAGCTGTATAGGCTTTTGCATAAG 2127
Db 1975 AATTTGTCAATAGTACAGAAATATTTGTCAAGAGGTAGTTTATACAGACTTTTGCATAAA 2034
QY 2128 TCAGGTGTCA---AAGACATAGATGAACACACGTGCAATGAATATGCTGTTTGAATGAGCA 2184
Db 2035 AGTGGAGCAAGGGAGCAATTAGATGAGAGACGTGCGCTGAGTATGGCTTATGATGTGGCT 2094
QY 2185 AAGGGAATGAACCTACCTCCACAGACGTGATCCTCCAATTTGTCATCGTGAATTTAAATCA 2244
Db 2095 AAGGGAATGAATATCTTCACAAATCGCAATCCTCCAATTTGTCATAGAGATCTAAATCT 2154
QY 2245 CCGAATCTGTTAGTTGACAAAGAAGTATACAGTCAAGGTTTGTGATTTTGGTCTCTCCCGT 2304
Db 2155 CCAAACTTATTTGTTGACAAAAATATACAGTCAAGGTTTGTGATTTTGGTCTCTCGCA 2214
QY 2305 TTAAAGGCACGCACATTTCTTTTCATCCAATCTGCAGCTGGAAACACCTGAATGATGGCA 2364
Db 2215 TTGAAGGCCAGCACGTTTCTTTCTCGAAGTCAGCAGCTGGAACCCCGAGTGGATGGCA 2274
QY 2365 CCAGAAGTACTACCGGATGAACCATCAAAATGAAAAAGTCAGATGTTTACAGCTTTGGAGTG 2424
Db 2275 CCAGAAGTCTTCGAGATGAGCCGCTCTAATGAAAAAGTCAGATGTTTACAGCTTCGGSGTC 2334
QY 2425 ATTTTGTGGAGTTGGCAACTTTTGAACAGCCCATGGTGTAAATCTAAACCCAGCTCAGGTT 2484

Db 2335 ATCTTGTGGAGCTTGTCTACATTGCAACAACCATGGGTAACCTAAATCCGGCTCAGGTT 2394
QY 2485 GTCCAGCTGTTGGATTAAAGGCAAAAGGCTTGACATCCCACGTTGATGTAATCCCAA 2544
Db 2395 GTAGTCCGGTTGGTTTCAAGTGTAAACGGCTGGAGATCCCGCGTAATCTGAATCCTCAG 2454
QY 2545 TTGGTTCCTTAATAGTGGCTTGTCTGGCCGATGAGCCATGGAACGTCCTTCTTTTCC 2604
Db 2455 GTTCAGCCATAATCGAGGTTGTTGGACCAATGAGCCATGGAAGCGTCCATCATTTGCA 2514
QY 2605 AGCATATGGAACCTTGAAACCAATGACTAAACAAGCGCCACCTCAACAAAGTCGCACA 2664
Db 2515 ACTAATAGGACTTGTCTAAGACCATTTGATCAATCAGCGGTTCTCCGCCCAACCGCTCG 2574
QY 2665 GA 2666
Db 2575 GA 2576

RESULT 3
US-08-003-311B-1
; Sequence 1, Application US/08003311B
; Patent No. 5444166
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene
; TITLE OF INVENTION: and Mutations
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
; ADDRESSEE: No. 5444166ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/003,311B
; FILING DATE: January 12, 1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/928,464
; FILING DATE: August 10, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lori Y. Bearell
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: UPN-1108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3033 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 118..2583
; US-08-003-311B-1

Query Match 27.4%; Score 898.8; DB 1; Length 3033;
Best Local Similarity 64.3%; Pred. No. 5.7e-227;
Matches 1582; Conservative 0; Mismatches 664; Indels 216; Gaps 7;

QY	253	AAAGGAGAAACCGATAGGGTTTTTTGATTGGGATGGGAGTGGTGATCACAGGTTAAACACGG	312
Db	283	AGAGCGGATTTGATTGGGATCCTAGCGGTGGTGGTGGTGATCATAGGTTGAATAAT	342
QY	313	CAGCGTATCGGATAGGGAACCTGT-----ATTCAATGGATTGGTTTACAGAGACATTCC	366
Db	343	CAACCGAATCGGGTTGGGAATAATATGTATGCTTCGTCTCTAGGGTTGCAAAGGCAATCC	402
QY	367	AGTGAAGCAGCTACGATGATAGCTCTCTCTAGTGATTACTACGCACCGACGCTATCA	426
Db	403	AGTGGAGTAGTTTCGGTGAGAGCTCTTTGTCTGGGATTATTATACATGCCTACGCTTTC-	461
QY	427	AACCTTCAGCAAAATGAGATCAATGCATTGGAATATATCCTCGATGATGATTTCCGAGTG	486
Db	462	--TGCGCGGCTAACGAGATCGAATCTGTTGGATTTCCTCAAGATGATGGGTTTAGGCTT	519
QY	487	ATGAAAGCTGTGGGAAGTCGAGGTTTCG-----	513
Db	520	GGATTGGTGGTGGAGGAGATTGAGGATACAGATGGCGGCGGACTCCGCTGGAGGG	579
QY	514	-----TCTGGAAGAGCTGGGCCACGACAGCGGAAGAGAGCTTTTCAGTTGCAGCAGCCC	567
Db	580	TCTTCATCTGGGAAGAGCTGGCGCGACAGACGGAGGAGATTATCAGCTGCAGCTTGCA	639
QY	568	TTGGTTCTTAGGCTTTCTTCAGATGNNACTTGTGCCGATGATCCCAACTTTATGGATCCG	627
Db	640	TTGGCGTTAAGGCTTTTCGTCCGAGGCTACTTGTGCCGACGATCCGAACTTTCTGGATCCT	699
QY	628	ATTCCAGACGAGGCAGCTTTTAAGATCGTTATCGATTTCAGCTGAGGCCATCTCGCATCGG	687
Db	700	GTACCGGACGAGCTTGCTTTACGGACTTCGCCAAGTTTCAGCCGAAACCGTTTCACATCGT	759
QY	688	TTCTGGTAAATGGATGCATGTCTATATTGGAGAAAAGTGCCAGATGGTTTTTATCTAATT	747
Db	760	TTCTGGGTTAATGGCTGCTTATCGTACTATGATAAAAGTTTCCTGATGGTTTTTATATGATG	819
QY	748	CATGGGATGGACCCCATATGTATGGTCATTATGACCAATCTGCAAGAGGATGGCGGTATA	807
Db	820	AATGCTCTGGATCCCTATATTTTGGACCTTATGTCATCGACCTGTCATGAAAGTGGTCGCATC	879
QY	808	CCATCATTTGAATCTCTGAAAACAGTTGATTCCAGCATCGGTTTCATCAATTGAAGTAGTT	867
Db	880	CTTCAATTGAATCATTAAGAGCTGTTGATTCTGGTGTGATTCTTCGTTGAAAGCGATC	939
QY	868	TTGATAGATCGGCATAGTGATGCTAGCTTTAAAGAACTGCAAAACAGGCTGCATAATATT	927
Db	940	ATAGTTGATAGCGTAGTGATCCAGCCTTCAGGAACTTCACAATAGAGTCCACGACATA	999
QY	928	TCTTCCAGTTGCTAAACCAACAAAGAGGTTGCAGATCATATAGCAAAAGCTGGTATGCAAT	987
Db	1000	TCTTGTAGCTGCATTACCACAAAGAGGTTGTTGATCAGCTGGCAAGCTTATCTGCAAT	1059
QY	988	CACTTGGGGGTTTCAGTTTCTGAGGGAGAAGATGACTTGGTTTCTGCCTGGAAGGAATGC	1047
Db	1060	CGTATGGGGGTTCCAGTTATCATGGGGGAAGATGAGTTGGTTCCCATGTGGAAGGAGTGC	1119
QY	1048	AGCGATGACTTAAAGGAATGTTTGGGATCTGCTGTGATTCCCTTATGCAGCTTATCTGTT	1107
Db	1120	ATTGATGGTCTAAAGAAATCTTTAAA---GTGGTGGTTCCCATAGGTAGCCTCTCTGTT	1176
QY	1108	GGCCTTTGTAGACATCGTGTCTCTTTTATTCAAAGTCCCTAGCTGATTCAATTGATTTACCC	1167
Db	1177	GGACTCTGCAGACATCGAGCTTTACTCTTCAAAGTACTGGCTGACATAATTGATTTACCC	1236
QY	1168	TGTCGAATTGCCAAAGGATGTAAATATTGTAATAGACCGATGCCGCTTCGTGCTTGTCT	1227
Db	1237	TGTCGAATTGCCAAAGGATGTAAATATTGTAATAGACCGATGCCGCTTCGTGCTTGTCT	1296
QY	1228	AGGTTTCGGCTTGATAGGGAATATCTCATCGATCTGATTGGGAGGCCAGGTTGCTTATGC	1287
Db	1297	AGGTTTCGGCTTGATAGGAGTACCTGGTTGATTTAGTAAAGAACCCAGGTCATTATGG	1356
QY	1288	CAACCTGATTTCTTTGCTCAATGGTCCCATCATCCATCTCAATTTCTTACCATTGGCATTT	1347

Db	1357	GAGCCTGATTCCTTGCTAAATGGTCCTTCATCTATCTCAATTCCTCTCTCTCGGGTTT	1416
QY	1348	CCAAGACTAAACCTATTGAATCTACCATGATTTCAGGTCAGTCCGCAACAGTATTTTC	1407
Db	1417	CCACGACCAAGCCAGTTGAACCCCGCAGTCGATTTTAGGTTACTAGCCAAACAATATTC	1476
QY	1408	TTGGATAGCCCAATCACCTTAATCTTGTTATTTGATGAAGCTTCCTTCAGGTAATGTTGTATCT	1467
Db	1477	TCCGATAGCCAGTCTCTTAATCTTGTTTCGATCCTGCATCAG	1519
QY	1468	GGGAAGGATGCTGCATTCCTCGGTCTATCAAAGGCCATTAAATAGGAAGGATGTAGATGGA	1527
Db	1520	----ATGATATGGGATTCCTCAATGTTTCATAGGCAATATGATAATCCGGGTGGAGAGAAT	1575
QY	1528	AAACCATAGTGGTTACTGGTGACAAGGACAGAAAATCTCAGTTATTAAATAAAAAGCA	1587
Db	1576	GACGCATTGGCAGAAAATGGTG	1597
QY	1588	GCCCAACTGAATACTCAAGATGGAAAGTCTGAGCAATTTAGATCATGTGTGCTTCTCTCCA	1647
Db	1598	-----	1597
QY	1648	TATAGTGTAAGTTCGAGCATCTCTTAGCATTTGTCTCATCCAAGGATGGATCATGTT	1707
Db	1598	-----GTGGGTCTTTGCCACCC	1614
QY	1708	ATTGGTTCTGAAGATTTCGGAGCATCTCTTAGCATTTGTCTCATCCAAGGATGGATCATGTT	1767
Db	1615	AGTGCTAATATGCTCCACAGAACATGATGGTGCCTCAAAATCAAATTTGAAGCAGCACCT	1674
QY	1768	AACAATTTACCAATTTGTTTCATGGTAGTCAGTTGATTAGAAAAACCAAAATGAGCTTTCCCTT	1827
Db	1675	ATGAATGCCCCACCAATCAGTCAGCCAGTTCAAAAACAGGGCAAAATAGGGAACCTTGGACTT	1734
QY	1828	GGCTTAGAAGATTGGTTATTCCATGGACAGATCTTGATTGAGGGAGAAAAATTTGGAGCA	1887
Db	1735	GATGGTGATGATGAGACATCCCGTGGTGTGATCTTAATATAAAAAGAAAAGATTGGAGCA	1794
QY	1888	GGTTCTTTTGGGACTGTATATCGTGGTAGTGGCATGGCTCTGATGTTGCTGTGAAGATC	1947
Db	1795	GGTTCTTTTGGCACTGTCCACCGTCTGAGTGGCATGGCTCGGATGTTGCTGTGAAGAT	1854
QY	1948	CTCACAGAACAAAGACTTCCATCCTGAAACGTGTTAATGAGTTTCTGAGAGAGGTTGCTATC	2007
Db	1855	CTCATGGAGCAAGACTTCCATGCTGAGCGTGTAAATGAGTTCTTAAGAGAGGTTGGGATA	1914
QY	2008	ATGAAATCTTTACGACATCCTAATATTGTACTGTTTATGGGTGCGGTGACCAAGCCACCA	2067
Db	1915	ATGAAACGCCCTTCGCCACCCCTAACATTGTTCTCTTCATGGTGGGTCTACTCAACCTCCA	1974
QY	2068	AACCTGTCCATTGTACCCGAATATCTATCGAGAGGTAGCTTGTATAGGCTTTTGCATAAG	2127
Db	1975	AATTGTCAATAGTGACAGAATATTTGTCAAGAGGTAGTTTATACAGACTTTTGCATAAA	2034
QY	2128	TCAGGTGTCA---AAGACATAGATGAACACCGTCGAAATAAATATGGCTTTTGTATGTGGCA	2184
Db	2035	AGTGGAGCAAGGGAGCAATTAGATGAGAGACGTGCGCTGAGTATGGCTTATGATGTGGCT	2094
QY	2185	AAGGGAAATGAACCTACTCCACAGACGTGATCCTCCAATTGTTTCATCGTGAATTTAAATCA	2244
Db	2095	AAGGGAAATGAATATCTTCAAAATCGCAATCCTCCAATTTGTGCATAGAGATCTAAAATCT	2154
QY	2245	CCGAATCTGTTAGTTGACAAGAAGTATACAGTCAAGGTTTGTGATTTTGGTCTCTCCCGT	2304
Db	2155	CCAAAACCTTATTGGTTGACAAAAAATATACAGTCAAGGTTTGTGATTTTGGTCTCTCGCGA	2214
QY	2305	TTAAAGGCACGCACATTTCTTTTCATCCAAATCTGAGCTGGAAACACCTGAATGGATGGCA	2364
Db	2215	TTGAAGGCCAGCACGTTTCTTTCTCGAAGTCAGCAGCTGGAAACCCCGAGTGGATGGCA	2274
QY	2365	CCAGAAGTACTACGCGATGAACCATCAAATGAAAAGTCAGATGTTTACAGCTTTGGAGTG	2424

Db 2275 CCAGAAAGTCCTGCGAGATGAGCCGCTTAATGAAAAAGTCAGATGTGTACAGCTTCGGGCTC 2334
Qy 2425 ATTTGTGGAGTTGGCAACTTTGCAACAGCCATGGTGTAAATCTAAACCCAGCTCAGGTT 2484
Db 2335 ATCTTGTGGAGCTTGCTACATTGCAACCAACCCATGGGTAACCTTAAATCCGGCTCAGGTT 2394
Qy 2485 GTCGCAGCTGTGGATTAAAGGCAAAAGGCTTGACATCCACCGTGTAAATCCCAA 2544
Db 2395 GTAGCTGCGGTGGTTTCAAGTGTAAACCGCTGGAGATCCCGGTAAATCTGAATCCTCAG 2454
Qy 2545 TTGGCTTCCTTAATAGTGGCTTGCTGGCCGATGAGCCATGGAACGTCCTTTTTC 2604
Db 2455 GTTGCAGCCATAATCGAGGGTTGTTGGACCAATGAGCCATGGAAGCGTCCATCATTTGCA 2514
Qy 2605 AGCATTATGAAACCTTGAAACCAATGACTAAACAGCGCCACCTCAACAAAGTCGCACA 2664
Db 2515 ACTATAATGAGACTTGCTAAGACCATTTGATCAATCAGCGGTTCTCCGCCCAACCGGCTCG 2574
Qy 2665 GA 2666
Db 2575 GA 2576

RESULT 4

US-08-261-432-1
; Sequence 1, Application US/08261432
; Patent No. 5602322
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene
; TITLE OF INVENTION: and Mutations
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
; ADDRESSEE: No. 5602322ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/261,432
; FILING DATE: June 17, 1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/003,311
; FILING DATE: January 12, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lori Y. Beardsell
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: UPN-1864
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3033 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 118..2583
US-08-261-432-1

Query Match.

27.4%; Score 898.8; DB 1; Length 3033;

Best Local Similarity 64.3%; Pred. No. 5.7e-227;
Matches 1582; Conservative 0; Mismatches 664; Indels 216; Gaps 7;
Qy 253 AAAGGGAGAACCGATAGGGTTTTTGGATGGGATGGGAGTGGTATCAGAGTTAAACACG 312
Db 283 AGAGGGGATTTCAATGGGATCCCTAGCGGTGGTGGTGGTATCATAGTTGAATAAT 342
Qy 313 CAGGCGTATCGGATAGGGAACCTGT-----ATTATGGATTGGTTTACAGAGACATTCC 366
Db 343 CAACCGAATCGGTTGGGAATAATATGTATGCTTCGTCTAGGTTGCAAGGCAATCC 402
Qy 367 AGTGAAGCAGCTACGATGATAGCTCTCTCTCTAGTATTAATACGACCGAGCTATCA 426
Db 403 AGTGGAGTAGTTTCGGTGAGAGCTCTTGTCTGGGATTAATACATGCTACGCTTTC- 461
Qy 427 AACCTGCAGCAATGAGATCAATGCAATGGAATATATCTCTGATGATGATTTCCGAGTG 486
Db 462 --TGCGGGCGGCTAACGAGATCGAATCTGTTGGATTCTCTCAAGATGATGGGTTTAGGCTT 519
Qy 487 ATGAAAGCTGTGGGAAGTGGAGTTCTG-----513
Db 520 GGATTTGGTGGTGGTGGAGGAGATTTGAGGATACAGATGGCGGGACTCCGCTGGAGGG 579
Qy 514 -----TCTGGAAGAGCTGGGCCCCAGCAGACGGAAGAGAGCTTTTCAGTTGCAGCAGCCC 567
Db 580 TCTTCATCTGGAAGAGCTGGGCGCAGCAGACGGAAGAGAGTTATCAGTGCAGCTTGCA 639
Qy 568 TTGGTTCTTAGGCTTTCTTCAGATGNNACTTGTGCCGATGATCCCAACTTTTATGGATCCG 627
Db 640 TTGGCGTTAAGGCTTTCGTGGAGGCTACTTGTGCCGACGATCCGAACCTTCTGGATCCT 699
Qy 628 ATTCCAGACGAGCAGCTTTAAGATCGTTATCGATTTCAGCTGAGGCCATCTCGCATCGG 687
Db 700 GTACCGGACGAGCTGCTTTACGAGCTTCGCCAAGTTCAGCCGAAACCGTTTCACATCGT 759
Qy 688 TTCTGGGTAATGGATGATGCTCATATTGAGAGAAAGTCCAGATGGTTTATCTAATT 747
Db 760 TTCTGGGTTAATGGCTGCTTATCGTACTATGATAAAGTTCCTGATGGGTTTATATGATG 819
Qy 748 CATGGATGGACCCATATGTATGTCTATTATGCACCAATCTGCAAGAGGATGGCGTATA 807
Db 820 AATGGTCTGGATCCCTATATTGACCTTATGATCGACCTGATGAAAGTGGTGGCATC 879
Qy 808 CCATCATTTGAATCTCTGAAACAGATTGATTCAGCAGATCGGTTTCATCAATTGAAGTAGTT 867
Db 880 CCTTCAATTGAATCATTAAGAGCTGTTGATTTCTGCTGTTGATTTCTTCGCTTGAAGCGATC 939
Qy 868 TTGATAGATCGCATAGTATGCTAGCTTAAAGAAAGTGCACAAACAGGCTGCATAATATT 927
Db 940 ATAGTTGATAGCGTAGTATCCAGCCTTCAAGGAATTCACAATAGAGTCCACGACATA 999
Qy 928 TCTTCCAGTTGTGTAAACCAAAAGAGGTTTGCAGATCATATAGCAAAAGCTGGTATGCAAT 987
Db 1000 TCTTGTAGCTGCATTACCACAAAAGAGGTTGTTGATCAGCTGGCAAAAGCTTATCTGCAAT 1059
Qy 988 CACTTGGGGGTTTCAGTTTCTGAGGGGAGAGATGACTTGGTTTCTGCTGGAAGGAAATGC 1047
Db 1060 CGTATGGGGGTTCCAGTTATCATGGGGGAGAGATGAGTTGGTTCCCATGTGGAAGGAGTGC 1119
Qy 1048 AGCGATGACTTAAAGGAATGTTGGGATCTGCTGTGATTCCTTATGAGCTTATCTGTT 1107
Db 1120 ATTGATGTTCTAAAGAAATCTTTAAA---GTGCTGGTTCCCATAGTAGCTCTCTCTGT 1176
Qy 1108 GGCCTTTGTAGACATCGTCTCTTTTATTCAAGTCCCTAGCTGATTCAATGATTTACCC 1167
Db 1177 GGACTCTGAGACATCGAGCTTACTCTTCAAGTACTGGCTGACATAATGATTTACCC 1236
Qy 1168 TGTCGAATGCCAAAGGATGTAATAATTGCACTAGAGATGATGCTTCATCTTGCCTTGT 1227
Db 1237 TGTCGAATGCCAAAGGATGTAATAATTGTAATAGAGACGATGCCGCTTCGTGCTTGTG 1296
Qy 1228 AGGTTCCGGCTTGATAGGGAATATCTCATCGATCTGATGGGAGGCGGAGGTTGCTTATGC 1287

Db 1297 AGGTTGGGCTTGATAGGAGTACCTGGTTGATTTAGTAGGAAAGCCAGGTCACATTATGG 1356

Qy 1288 CAACCTGATCTTTTGTCTCAATGGTCCATCATCTCAATTTCTTCCACATTGCGATTT 1347

Db 1357 GAGCCTGATCTCTGTAAATGGTCCCTCATCTATCTCAATTTCTTCTCCTCTGCGGTTT 1416

Qy 1348 CCAAGACTAAACCTATTGAATCTACCAATTGATTTTCAGGTCACCTGGCCAAACAGTATTC 1407

Db 1417 CCACGACCAAGCCAGTTGAACCCGAGTCGATTTTAGGTTACTAGCCAAACAATATTC 1476

Qy 1408 TTGGATAGCCCAATCATTAACTTCTGATTTTGAATGAAGCTTCTTCAGGTAATGTTGTATCT 1467

Db 1477 TCCGATAGCCAGTCTCTTAATCTTGTCTTCGATCCTGCATCAG----- 1519

Qy 1468 GCGAAGGATGCTGCATCTCCGTCTATCAAGGCCATTAAATAGGAAGGATGTAGATGGA 1527

Db 1520 ----ATGATATGGGATCTCAATGTTTCATAGGCAATATGATAATCCGGGTGGAGAGAA 1575

Qy 1528 AAAACCATAGTGGTTACTGGTGACAAGGACAGAAATCTCAGTTATTAAATAAAAGCA 1587

Db 1576 GACGCATTGGCAGAAAATGGTG----- 1597

Qy 1588 GCCCAACTGAATACTCAAGATGGAAGTCTGAGCAATTTAGATCATGTGTTGTTCTTCCA 1647

Db 1598 ----- 1597

Qy 1648 TATAGTGACAGTCGACCCCTTTTGTAGAAAATGTAGTCCCTTTAAGCCATATCTCACAC 1707

Db 1598 -----GTGGGTCTTTGCCACCC 1614

Qy 1708 ATTGGTTCTGAAGATTCGGAGCATCTCTTAGCATGTCTCATCCAGGATGGATCATGTT 1767

Db 1615 AGTGCTAAATATGCCCTCCACAGAAACATGATGCGTCGTCAAATCAAAATGAAGCAGCACCT 1674

Qy 1768 AACAAATTACCAATTTGTTTCATGGTAGTCAGTTGANTAGAAAACCAAAATGAGCTTTCCCTT 1827

Db 1675 ATGAATGCCCCACCAATCAGTCAGCCAGTTCCTCAACAGGGCAATAGGGAACTTTGGACTT 1734

Qy 1828 GGCTTAGAAGATTTGTTTATTCATGGACAGATCTTGATTGAGGAGAGAAAATTTGGAGCA 1887

Db 1735 GATGGTGATGATATGGACATCCCGTGGTGTGATCTTAATATAAAAGAAAAGATTGGAGCA 1794

Qy 1888 GGTCTTTTGGGACTGTATATCGTGGTGAGTGGCATGGCTCTGATGTGCTGTGAAGATC 1947

Db 1795 GGTCTCTTTGGCAGCTGTCCACCGTCTGAGTGGCATGGCTCGGATGTGCTGTGAAAATT 1854

Qy 1948 CTCACAGAACAAAGACTTCCATCCTGAACGTTAATGAGTTTCTGAGAGAGGTTGCTATC 2007

Db 1855 CTCATGGAGCAAGACTTCCATGCTGAGCGTGTAAATGAGTTCTTAAGAGAGGTTGCGATA 1914

Qy 2008 ATGAAATCTTTACGACATCTCTAATATTGTACTGTTTATGGTGCGGTGACCAAGCCACCA 2067

Db 1915 ATGAAACGCCTTCGCCACCTTAACATTGTTCTCTTCTATGGGTGCGGTCACTCAACCTCCA 1974

Qy 2068 AACTTGTCCATTGTCACCGAATATCTATCGAGAGGTAGCTTGATAGGCTTTTGCATAAG 2127

Db 1975 AATTTGTCAATAGTGACAGATAATTGTCAGAGGAGGTAGTTTATACAGACTTTTGCATAAA 2034

Qy 2128 TCAGGTGTCA---AAGACATAGATGAAACACAGTCGAATAAATATGGCTTTTGTATGAGCA 2184

Db 2035 AGTGGAGCAAGGAGCAATTAGATGAGAGACGTCGCTGAGTATGGCTTATGATGTGGCT 2094

Qy 2185 AAGGGAATGAACACTACCTCCACAGACGTCATCCCAATGTTTCATCGTGAATTTAAATCA 2244

Db 2095 AAGGGAATGAATTATCTTCACAATCGCAATCCCAATGTCATGATAGATCTAAATCT 2154

Qy 2245 CCGAATCTGTAGTTGACAGAAGTATACAGTCAAGGTTTGTGATTTTGGTCTCTCCCGT 2304

Db 2155 CCAAACTTATTGGTTGACAAAAAATATACAGTCAAGGTTTGTGATTTTGGTCTCTCGCGA 2214

Qy 2305 TTAAGGCAGGCACATTTCTTTCATCCAAATCTGCAGCTGGAACACCTGAATGGATGGCA 2364

Db 2215 TTGAAGGCCAGCACGTTTCTTCTCGAAGTCAAGAGCTGGAACCCCGAGTGGATGGCA 2274

Qy 2365 CCAGAAGTACTACGCGATGAACCATCAAAATGAAAAAGTCAGATGTTTACAGCTTTGGAGTG 2424

Db 2275 CCAGAAGTCTCGGAGATGAGCCGTCTAATGAAAAAGTCAGATGTTTACAGCTTCGGGGTC 2334

Qy 2425 ATTTGTGGGAGTTGGCAACTTTTGCAACAGCCATGGTGTAAATCTAAACCCAGCTCAGGTT 2484

Db 2335 ATCTGTGGGAGCTTGCTACATGCAACCAACCATGGGTAACTTAAATCCGGCTCAGGTT 2394

Qy 2485 GTGCAGCTGTTGGATTAAAGGGCAAAAAGGCTTGACATCCCACGTCATGATGTAATCCCAA 2544

Db 2395 GTAGTGGGTTGGTTTCAAGTGTAAACGGCTGGAGATCCCGCGTAATCTGAATCCTCAG 2454

Qy 2545 TTGGCTTCCTTAATAGTGGCTTGCTGGCCGATGAGCCATGGAACGTCCTTCTTTTTC 2604

Db 2455 GTTGAGCCATAATCGAGGTTGTTGGACCAATGAGCCATGGAAGCGTCCATCATTTGCA 2514

Qy 2605 AGCATATGGAACCTTGAAACCAATGACTAAACAAAGCGCCACCTCAACAAAAGTCGCACA 2664

Db 2515 ACTAATATGGACTTGCTAAGACCATTTGATCAATCAGCGGTTCTCTCGCCCAACCGCTCG 2574

Qy 2665 GA 2666

Db 2575 GA 2576

RESULT 5

US-07-928-464-4

; Sequence 4, Application US/07928464

; Patent No. 5367065

; GENERAL INFORMATION:

; APPLICANT: Ecker, Joseph R.

; APPLICANT: Kieber, Joseph J.

; TITLE OF INVENTION: Constitutive Triple Response Gene and

; TITLE OF INVENTION: Mutations

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and

; ADDRESSEE: No. 5367065ris

; STREET: One Liberty Place - 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: U.S.A.

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/928,464

; FILING DATE: 19920810

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Miller, Suzanne E.

; REGISTRATION NUMBER: 32,279

; REFERENCE/DOCKET NUMBER: UPN-1086

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-568-3100

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5873 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-07-928-464-4

Query Match 4.7%; Score 155.2; DB 1; Length 5873;

Best Local Similarity 69.4%; Pred. No. 6.5e-31;

Matches 211; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

Qy 693 GGTAATGATGTCATGTCATATTGGAGAAAGTCCAGATGGTTTTTATCTAATTCATGG 752

Db 1176 GGTTAATGGCTGCTTATCGTACTATGATAAAGTTCCTGATGGGTTTATATGATGAATGG 1235
QY 753 GATGGACCCATATGATGGTCACTATATGCACCAATCTGCAAGAGGATGGCGGTATACCATC 812
Db 1236 TCTGGATCCCTATATTTGGACCTTATGCATCGACCTGCATGAAAGTGGTGGCATCCCTTC 1295
QY 813 ATTTGAATCTCTGAAAACAGTTGATTCAGCATCGGTTTCATCAATTGAAGTAGTTTGTAT 872
Db 1296 AATTGAATCATTAAAGAGCTGTGATTCCTGGTGTGATTCCTCGCTTGAAGCGATCATAGT 1355
QY 873 AGATCGGCATAGTGTGATTCAGCATCGGTTTCATCAATTGAAGTAGTTTGTAT 932
Db 1356 TGATAGGCGTAGTGCACGCCCTTCAAGGAACCTTCAATAGAGTCCACGACATATCTTG 1415
QY 933 CAGTTGTGTAACCAACAAAGAGTTGCAGATCATATAGCAAAAGCTGGTATGCAATCACTT 992
Db 1416 TAGCTGCATTACCAACAAAGAGTTGTTGATCAGCTGGCAAGCTTATCTGCAATCGTAT 1475
QY 993 GGGG 996
Db 1476 GGGG 1479

RESULT 6
PCT-US93-07347-4
; Sequence 4, Application PC/TUS9307347
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene and
; TITLE OF INVENTION: Mutations
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
; ADDRESSEE: Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07347
; FILING DATE: 19930805
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Suzanne E.
; REGISTRATION NUMBER: 32,279
; REFERENCE/DOCKET NUMBER: UPN-1086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5873 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US93-07347-4

Query Match 4.7%; Score 155.2; DB 5; Length 5873;
Best Local Similarity 69.4%; Pred. No. 6.5e-31;
Matches 211; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
QY 693 GGTAATGGATGCATGTCTATTTGGAGAAAGTGCAGATGGTTTTTATCTAATTCATGG 752
Db 1176 GGTTAATGGCTGCTTATCGTACTATGATAAAGTTCCTGATGGGTTTATATGATGAATGG 1235

QY 753 GATGGACCCATATGATGGTCACTATATGCACCAATCTGCAAGAGGATGGCGGTATACCATC 812
Db 1236 TCTGGATCCCTATATTTGGACCTTATGCATCGACCTGCATGAAAGTGGTGGCATCCCTTC 1295
QY 813 ATTTGAATCTCTGAAAACAGTTGATTCAGCATCGGTTTCATCAATTGAAGTAGTTTGTAT 872
Db 1296 AATTGAATCATTAAAGAGCTGTGATTCCTGGTGTGATTCCTCGCTTGAAGCGATCATAGT 1355
QY 873 AGATCGGCATAGTGTGATTCAGCATCGGTTTCATCAATTGAAGTAGTTTGTAT 932
Db 1356 TGATAGGCGTAGTGCACGCCCTTCAAGGAACCTTCAATAGAGTCCACGACATATCTTG 1415
QY 933 CAGTTGTGTAACCAACAAAGAGTTGCAGATCATATAGCAAAAGCTGGTATGCAATCACTT 992
Db 1416 TAGCTGCATTACCAACAAAGAGTTGTTGATCAGCTGGCAAGCTTATCTGCAATCGTAT 1475
QY 993 GGGG 996
Db 1476 GGGG 1479

RESULT 7
US-07-928-464-3
; Sequence 3, Application US/07928464
; Patent No. 5367065
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene and
; TITLE OF INVENTION: Mutations
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
; ADDRESSEE: No. 5367065ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/928,464
; FILING DATE: 19920810
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Suzanne E.
; REGISTRATION NUMBER: 32,279
; REFERENCE/DOCKET NUMBER: UPN-1086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5890 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1..353
; FEATURE:
; NAME/KEY: exon
; LOCATION: 354..1001
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1002..1176
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1177..1477

FEATURE: intron
NAME/KEY: 1478..1574
LOCATION:
FEATURE: exon
NAME/KEY: 1575..1719
LOCATION:
FEATURE: intron
NAME/KEY: 1720..1936
LOCATION:
FEATURE: exon
NAME/KEY: 1937..2038
LOCATION:
FEATURE: intron
NAME/KEY: 2039..2173
LOCATION:
FEATURE: exon
NAME/KEY: 2174..2379
LOCATION:
FEATURE: intron
NAME/KEY: 2380..2736
LOCATION:
FEATURE: exon
NAME/KEY: 2737..3012
LOCATION:
FEATURE: intron
NAME/KEY: 3013..3202
LOCATION:
FEATURE: exon
NAME/KEY: 3203..3243
LOCATION:
FEATURE: intron
NAME/KEY: 3244..3519
LOCATION:
FEATURE: exon
NAME/KEY: 3520..3588
LOCATION:
FEATURE: intron
NAME/KEY: 3589..3668
LOCATION:
FEATURE: exon
NAME/KEY: 3669..3769
LOCATION:
FEATURE: intron
NAME/KEY: 3770..3858
LOCATION:
FEATURE: exon
NAME/KEY: 3859..3943
LOCATION:
FEATURE: intron
NAME/KEY: 3944..4037
LOCATION:
FEATURE: exon
NAME/KEY: 4038..4136
LOCATION:
FEATURE: intron
NAME/KEY: 4137..4369
LOCATION:
FEATURE: exon
NAME/KEY: 4370..4438
LOCATION:
FEATURE: intron
NAME/KEY: 4439..4541
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FEATURE: exon
NAME/KEY: 4542..4673
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FEATURE: intron
NAME/KEY: 4674..4787
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FEATURE: exon
NAME/KEY: 4788..4882
LOCATION:
FEATURE:

NAME/KEY: intron
LOCATION: 4883..4959
FEATURE:
NAME/KEY: exon
LOCATION: 4960..5056
FEATURE:
NAME/KEY: intron
LOCATION: 5057..5890
US-07-928-464-3
Query Match 4.7%; Score 155.2; DB 1; Length 5890;
Best Local Similarity 69.4%; Pred. No. 6.5e-31;
Matches 211; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
QY 693 GGTAAATGGATGCATGTCATATTTGGAGAAAGTCCAGATGGTTTTTATCTAATTCATGG 752
Db |||||
1176 GGTAAATGGCTGCTTATCGTACTATGATAAAAGTTCTTGATGGGTTTATATGATGAATGG 1235
QY 753 GATGACCCCATATGATGGTCATTATGCACCAANTCTGCAAGAGGATGGCGGTATACCATC 812
Db |||||
1236 TCTGGATCCCTATATTGGACCTTATGCATCGACCTGCATGAAAGTGGTCGCATCCCTTC 1295
QY 813 ATTTGAATCTCTGAAAAACAGTTGATTCACCATCGGTTTCATCAATTGAAGTAGTTTIGAT 872
Db |||||
1296 AATTGAATCATTAAAGACCTGTTGATTTCTGCTGTTGATTTCTCGCTTGAAGCGATCATAGT 1355
QY 873 AGATCGGCATAGTGTAGTCTAGCTTAAAGAACTGCAAAACAGGGTGCATAATATTTCTTC 932
Db |||||
1356 TGATAGCGGTAGTGTCCAGCCTTCAAGGAACTTCACAAATAGAGTCCACGACATATCTTG 1415
QY 933 CAGTTGTGTAAACCACAAAGAGGTTGCAGATCATATAGCAAAGCTGGTATGCAATCACTT 992
Db |||||
1416 TAGCTGCATTACCAACAAAGAGGTTGTTGTATCAGCTGGCAAAGCTTATCTGCAATCGTAT 1475
QY 993 GGGG 996
Db 1476 GGGG 1479

RESULT 8
US-07-928-464-5
Sequence 5, Application US/07928464
Patent No. 5367065
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene and
TITLE OF INVENTION: Mutations
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
ADDRESSEE: No. 5367065ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/928,464
FILING DATE: 19920810
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Suzanne E.
REGISTRATION NUMBER: 32,279
REFERENCE/DOCKET NUMBER: UPN-1086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 5:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 5890 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-928-464-5

Query Match          4.7%; Score 155.2; DB 1; Length 5890;
Best Local Similarity 69.4%; Pred. No. 6.5e-31;
Matches 211; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 693 GGTAATGGATGCATGTCTATATTGGAGAAAGTCCAGATGGTTTTTATCTAATTCATGG 752
Db 1176 GGTTAATGGCTGCTTATCGTACTATGATAAAGTTCCTGATGGTTTTTATATGATGAATGG 1235
QY 753 GATGGACCCATATGTATGGTCAATATGACCAATCTGCAAGAGGATGGCGTATACCATC 812
Db 1236 TCTGGATCCCTATATTGGACCTTATGATCGACCTGATGAAAGTGGTCGCATCCCTTC 1295
QY 813 ATTTGAATCTCTGAAAACAGTTGATTCAGCATCGGTTTCATCAATTGAAGTAGTTTGTAT 872
Db 1296 AATTGAATCAATAAGAGCTGTTGATTCGTTGTTGATTCCTGTTGAAGCGATCATAGT 1355
QY 873 AGATCGGCATAGTGCTAGCTTAAAGAACTGCAAAACAGGGTGCAATAATTTCTTC 932
Db 1356 TGATAGCGGTAGTGATCCAGCCTTCAAGGAACCTTCAATAGAGTCCACGACATATCTTG 1415
QY 933 CAGTTGTGTAAACACAAAAGAGGTTGCAGATCATATAGCAAGCTGGTATGCAATCACTT 992
Db 1416 TAGCTGCATTACCAAAAAGAGGTTGTTGATCAGCTGGCAAGCTTATCTGCAATCGTAT 1475
QY 993 GGGG 996
Db 1476 GGGG 1479
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RESULT 9
PCT-US93-07347-3
; Sequence 6, Application US/07928464
; Patent No. 5367065
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene and
; TITLE OF INVENTION: Mutations
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
; ADDRESSEE: No. 5367065ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/928,464
; FILING DATE: 19920810
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Suzanne E.
; REGISTRATION NUMBER: 32,279
; REFERENCE/DOCKET NUMBER: UPN-1086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5890 base pairs
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; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-928-464-6

Query Match          4.7%; Score 155.2; DB 1; Length 5890;
Best Local Similarity 69.4%; Pred. No. 6.5e-31;
Matches 211; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 693 GGTAATGGATGCATGTCTATATTGGAGAAAGTCCAGATGGTTTTTATCTAATTCATGG 752
Db 1176 GGTTAATGGCTGCTTATCGTACTATGATAAAGTTCCTGATGGTTTTTATATGATGAATGG 1235
QY 753 GATGGACCCATATGTATGGTCAATATGACCAATCTGCAAGAGGATGGCGTATACCATC 812
Db 1236 TCTGGATCCCTATATTGGACCTTATGATCGACCTGATGAAAGTGGTCGCATCCCTTC 1295
QY 813 ATTTGAATCTCTGAAAACAGTTGATTCAGCATCGGTTTCATCAATTGAAGTAGTTTGTAT 872
Db 1296 AATTGAATCAATAAGAGCTGTTGATTCGTTGATTCCTGTTGAAGCGATCATAGT 1355
QY 873 AGATCGGCATAGTGCTAGCTTAAAGAACTGCAAAACAGGGTGCAATAATTTCTTC 932
Db 1356 TGATAGCGGTAGTGATCCAGCCTTCAAGGAACCTTCAATAGAGTCCACGACATATCTTG 1415
QY 933 CAGTTGTGTAAACACAAAAGAGGTTGCAGATCATATAGCAAGCTGGTATGCAATCACTT 992
Db 1416 TAGCTGCATTACCAAAAAGAGGTTGTTGATCAGCTGGCAAGCTTATCTGCAATCGTAT 1475
QY 993 GGGG 996
Db 1476 GGGG 1479
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RESULT 10
PCT-US93-07347-3
; Sequence 3, Application PC/TUS9307347
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene and
; TITLE OF INVENTION: Mutations
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
; ADDRESSEE: Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07347
; FILING DATE: 19930805
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Suzanne E.
; REGISTRATION NUMBER: 32,279
; REFERENCE/DOCKET NUMBER: UPN-1086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5890 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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1	1	MOLECULE TYPE:	DNA (genomic)
2	2	FEATURE:	
3	3	NAME/KEY:	intron
4	4	LOCATION:	1..353
5	5	FEATURE:	
6	6	NAME/KEY:	exon
7	7	LOCATION:	354..1001
8	8	FEATURE:	
9	9	NAME/KEY:	intron
10	10	LOCATION:	1002..1176
11	11	FEATURE:	
12	12	NAME/KEY:	exon
13	13	LOCATION:	1177..1477
14	14	FEATURE:	
15	15	NAME/KEY:	intron
16	16	LOCATION:	1478..1574
17	17	FEATURE:	
18	18	NAME/KEY:	exon
19	19	LOCATION:	1575..1719
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22	22	LOCATION:	1720..1936
23	23	FEATURE:	
24	24	NAME/KEY:	exon
25	25	LOCATION:	1937..2038
26	26	FEATURE:	
27	27	NAME/KEY:	intron
28	28	LOCATION:	2039..2173
29	29	FEATURE:	
30	30	NAME/KEY:	exon
31	31	LOCATION:	2174..2379
32	32	FEATURE:	
33	33	NAME/KEY:	intron
34	34	LOCATION:	2380..2736
35	35	FEATURE:	
36	36	NAME/KEY:	exon
37	37	LOCATION:	2737..3012
38	38	FEATURE:	
39	39	NAME/KEY:	intron
40	40	LOCATION:	3013..3202
41	41	FEATURE:	
42	42	NAME/KEY:	exon
43	43	LOCATION:	3203..3243
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45	45	NAME/KEY:	intron
46	46	LOCATION:	3244..3519
47	47	FEATURE:	
48	48	NAME/KEY:	exon
49	49	LOCATION:	3520..3588
50	50	FEATURE:	
51	51	NAME/KEY:	intron
52	52	LOCATION:	3589..3668
53	53	FEATURE:	
54	54	NAME/KEY:	exon
55	55	LOCATION:	3669..3769
56	56	FEATURE:	
57	57	NAME/KEY:	intron
58	58	LOCATION:	3770..3858
59	59	FEATURE:	
60	60	NAME/KEY:	exon
61	61	LOCATION:	3859..3943
62	62	FEATURE:	
63	63	NAME/KEY:	intron
64	64	LOCATION:	3944..4037
65	65	FEATURE:	
66	66	NAME/KEY:	exon
67	67	LOCATION:	4038..4136
68	68	FEATURE:	
69	69	NAME/KEY:	intron
70	70	LOCATION:	4137..4369
71	71	FEATURE:	
72	72	NAME/KEY:	exon
73	73	LOCATION:	4370..4438

/	FEATURE:				
/	NAME/KEY:	intron			
/	LOCATION:	4439..4541			
/	FEATURE:				
/	NAME/KEY:	exon			
/	LOCATION:	4542..4673			
/	FEATURE:				
/	NAME/KEY:	intron			
/	LOCATION:	4674..4787			
/	FEATURE:				
/	NAME/KEY:	exon			
/	LOCATION:	4788..4882			
/	FEATURE:				
/	NAME/KEY:	intron			
/	LOCATION:	4883..4959			
/	FEATURE:				
/	NAME/KEY:	exon			
/	LOCATION:	4960..5056			
/	FEATURE:				
/	NAME/KEY:	intron			
/	LOCATION:	5057..5890			
/	PCT-US93-07347-3				
	Query Match	4.7%;	Score 155.2;	DB 5;	Length 5890;
	Best Local Similarity	69.4%;	Pred. No. 6.5e-31;		
	Matches 211;	Conservative 0;	Mismatches 93;	Indels 0;	Gaps 0;
QY	693	GGTAAATGATGCATGTTCATATTTTGGAGAAAAGTGCCAGATGGTTTTTTTATCTAATTCATGG	752		
Db	1176	GGTTAATGGCTGCTTATCGTACTATGATAAAGTTCCTGATGGGTTTTTATATGATGAATGG	1235		
QY	753	GATGGACCCATATGTATGGTCATTATGCACCAATCTGCAAGAGGATGGCGGTATACCATC	812		
Db	1236	TCTGGATCCCTATATTTTGGACCTTATGCATCGACCTGCATGAAAGTGGTCGCATCCCTTC	1295		
QY	813	ATTGGAATCTGTAAAAACAGTTGATTCACGATCGGTTTCATCAATTGAAGTAGTTTGAT	872		
Db	1296	AATTGAATCATTAAGAGCTGTTGATTTCTGGTGTGTGATTTCTTCGCTTGAAGCGATCATAGT	1355		
QY	873	AGATCGGCATAGTATGCTAGCTTAAAGAAGTGC AAAACAGGGTGCATAATATTCTTC	932		
Db	1356	TGATAGCGGTAGTATCCAGCCTTCAAGGAACCTCACAAATAGAGTCCACGACATATCTTG	1415		
QY	933	CAGTTGTGTAAACCAAAAGAGGTTGCAGATCATATAGCAAAGCTGGTATGCCAATCACTT	992		
Db	1416	TAGCTGCATTACCAAAAAGAGGTTGTTGATCAGCTGGCAAAGCTTATCTGCAATCGIAT	1475		
QY	993	GGGG 996			
Db	1476	GGGG 1479			

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RESULT 11
PCT-US93-07347-5
; Sequence 5, Application PC/TUS9307347
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene and
; TITLE OF INVENTION: Mutations
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
; ADDRESSEE: Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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PRIOR APPLICATION DATA: 07/928,464
APPLICATION NUMBER: 07/928,464
FILING DATE: August 10, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: UPN-1108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6295 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-003-311B-4

Query Match 4.7%; Score 155.2; DB 1; Length 6295;
Best Local Similarity 69.4%; Pred. No. 6.7e-31;
Matches 211; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
QY 693 GGTAAATGGATGTCATATTTGGAGAAAGTCCAGATGGTTTTTATCTAATTCATGG 752
Db 1598 GGTAAATGGCTGCTTATCGTACTATGATAAAGTTCTGTATGGGTTTTATATGATGAATGG 1657
QY 753 GATGGACCCATATGTCATGTCATTTGACCTTATGTCATGCAAGAGGATGGCGGTATACCATC 812
Db 1658 TCTGGATCCCTATATTTGGACCTTATGTCATGCAAGAGGATGGTCCGATCCCTTC 1717
QY 813 ATTTGAATCTCTGAAACAGTTGATTCAGCATCGGTTTCATCAATTTGAAGTAGTTTGTAT 872
Db 1718 AATTGAATCATTAAAGAGCTGTTGATTCGTTGATTTCTCGTTGAAGCGATCATAGT 1777
QY 873 AGATCGGCATAGTCATGCTAGCTTTAAAGAACTGCAAAACAGGGTGCATAATATTTCTTC 932
Db 1778 TGATAGCGGTAGTCATCCAGCTTCAAGAACTTCACAATAGAGTCCACGACATATCTTG 1837
QY 933 CAGTTGTGTAAACCAAAAGAGGTTGCAGATCATATAGCAAGCTGGTATGCAATCACTT 992
Db 1838 TAGCTGCATTACCAAAAGAGGTTGTTGATCAGCTGGCAAGCTTATCTGCAATCGTAT 1897
QY 993 GGGG 996
Db 1898 GGGG 1901

RESULT 14
US-08-261-432-4
Sequence 4, Application US/08261432
Patent No. 5602322
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene
TITLE OF INVENTION: and Mutations
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: No. 5602322ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,432

FILING DATE: June 17, 1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/003,311
FILING DATE: January 12, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: UPN-1864
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6295 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-261-432-4

Query Match 4.7%; Score 155.2; DB 1; Length 6295;
Best Local Similarity 69.4%; Pred. No. 6.7e-31;
Matches 211; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
QY 693 GGTAAATGGATGTCATATTTGGAGAAAGTCCAGATGGTTTTTATCTAATTCATGG 752
Db 1598 GGTAAATGGCTGCTTATCGTACTATGATAAAGTTCTGTATGGGTTTTATATGATGAATGG 1657
QY 753 GATGGACCCATATGTCATGTCATTTGACCAATCTGCAAGAGGATGGCGGTATACCATC 812
Db 1658 TCTGGATCCCTATATTTGGACCTTATGTCATGCAAGAGGATGGTCCGATCCCTTC 1717
QY 813 ATTTGAATCTCTGAAACAGTTGATTCAGCATCGGTTTCATCAATTTGAAGTAGTTTGTAT 872
Db 1718 AATTGAATCATTAAAGAGCTGTTGATTCGTTGATTTCTCGTTGAAGCGATCATAGT 1777
QY 873 AGATCGGCATAGTCATGCTAGCTTTAAAGAACTGCAAAACAGGGTGCATAATATTTCTTC 932
Db 1778 TGATAGCGGTAGTCATCCAGCTTCAAGAACTTCACAATAGAGTCCACGACATATCTTG 1837
QY 933 CAGTTGTGTAAACCAAAAGAGGTTGCAGATCATATAGCAAGCTGGTATGCAATCACTT 992
Db 1838 TAGCTGCATTACCAAAAGAGGTTGTTGATCAGCTGGCAAGCTTATCTGCAATCGTAT 1897
QY 993 GGGG 996
Db 1898 GGGG 1901

RESULT 15
US-08-003-311B-3
Sequence 3, Application US/08003311B
Patent No. 5444166
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene
TITLE OF INVENTION: and Mutations
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: No. 5444166ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1

Sat Oct 25 11:01:50 2003

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/003,311B
; FILING DATE: January 12, 1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/928,464
; FILING DATE: August 10, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lori Y. Beardell
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: UPN-1108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6312 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-003-311B-3

Query Match      4.7%; Score 155.2; DB 1; Length 6312;
Best Local Similarity 69.4%; Pred. No. 6.7e-31;
Matches 211; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY      693  GGTAATGGATGCATGTATATTTGGAGAAAAGTGCCAGATGGTTTTTATCTAATTCATGG 752
Db      1598  GGTTAATGGCTGCTTATCGTACTATGATAAAAGTTCCTGATGGGTTTTTATATGATGAATGG 1657

QY      753  GATGGACCCATATGTATGGTCAATATGCACCAATCTGCAAGAGGATGGCGGTATACCATC 812
Db      1658  TCTGGATCCCTATATTTGGACCTTATGCATCGACCTGCATGAAAGTGGTCGCATCCCTTC 1717

QY      813  ATTTGAATCTCTGAAAAACAGTTGATTCAGCATCGGTTCAATCAATTGAAGTAGTTTGAT 872
Db      1718  AATTGAATCATTAAAGAGCTGTTGATTCTGGTGTGATTCTCGCTTGAAGCGATCATAGT 1777

QY      873  AGATCGGCATAGTGATGCTAGCTTAAAGAACTGCAAAACAGGCTGCATAATATTCTTC 932
Db      1778  TGATAGGCGTAGTGATCCAGCCTTCAAGGAACTTCACAATAGAGTCCACGACATATCTTG 1837

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QY      993  GGGG 996
Db      1898  GGGG 1901
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Search completed: October 24, 2003, 05:12:29
Job time : 200 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: October 24, 2003, 04:53:49 ; Search time 837 Seconds
(without alignments)
10528.552 Million cell updates/sec

Title: US-09-904-389-1
Perfect score: 3286
Sequence: 1 attcgatttcggaagaga.....aaaaaaaaaaaaaaaa 3286

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues
Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	412	12.5	2892	10	US-09-938-842A-1073
4	296.4	9.0	2661	10	US-09-938-842A-1085
5	270.2	8.2	2211	10	US-09-938-842A-1577
6	141.6	4.3	255	10	US-09-878-574-10192
7	136.6	4.2	397	10	US-09-878-574-46
8	136	4.1	1662	10	US-09-938-842A-1014
9	111.8	3.4	1638	10	US-09-938-842A-903
10	84.8	2.6	246	9	US-09-923-876-1947
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15	72.6	2.2	2975	12	US-10-440-341-2
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18	72.6	2.2	2977	14	US-10-057-550-25	Sequence 25, Appli
19	72.6	2.2	2977	14	US-10-173-225B-64	Sequence 64, Appli
20	72.4	2.2	1428	10	US-09-938-842A-882	Sequence 882, App
21	72.2	2.2	2640	10	US-09-938-842A-1270	Sequence 1270, Ap
22	71.8	2.2	2505	10	US-09-947-199-3	Sequence 3, Appli
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ALIGNMENTS

RESULT 1

US-09-904-389-1
; Sequence 1, Application US/09904389
; Patent No. US20020129404A1
; GENERAL INFORMATION:
; APPLICANT: Clendennen, Stephanie K.
; APPLICANT: Schuster, Debra K.
; TITLE OF INVENTION: CTR1 HOMOLOGUE FROM MELON
; FILE REFERENCE: 4257-0029.30
; CURRENT APPLICATION NUMBER: US/09/904,389
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 60/218,307
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3286
; TYPE: DNA
; ORGANISM: Cucumis melo
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (81)...(81)
; OTHER INFORMATION: n = A,T,C or G
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US-09-904-389-1

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Matches 3286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2665 GA 2666

Db 2458 GA 2459

RESULT 3

US-09-938-842A-1073
; Sequence 1073, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1073
; LENGTH: 2892
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1073

Query Match 12.5%; Score 412; DB 10; Length 2892;
Best Local Similarity 53.2%; Pred. No. 7.5e-102;
Matches 1069; Conservative 0; Mismatches 855; Indels 84; Gaps 6;

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QY 848 GTTCATCAATTGAAGTAGTTTGTATAGATCGGCATAGTGTATGCTTAGCTTTAAAGAACTGC 907
Db 1010 ATACATCAATGGAAGTGGTTTGTATAGATAGACGCTGAGACTCACGTCTTAAAGAACTGG 1069
QY 908 AAAACAGGGTGCATAAATTTCTCCAGTTGTGTAAACCAAAAAGAGGTTGCAGATCATTA 967
Db 1070 AGGATAAGGCACATGAGCTGTATTGTTCTTCAGACAACATGTTAGTCTCTCGAGAAAC 1129
QY 968 TAGCAAAGCTGGTATGCAATCACTTTGGGGGTTTCAGTTTCTGAGGGAGAGATGACTTGG 1027
Db 1130 TTGGCAGACTTGTTCGGTCTATATGGGGGGGAATTTCCAGGTGGAGCAAGTGAATCTCC 1189
QY 1028 TTTCTGCTGGAAGGAATGCAGCGATGACTTAAAGGAATGTTTGGGATCTGCTGTGATTC 1087
Db 1190 AGAAACGATGGAACACTGGTCAGCAATAGACTCAAGGAATTTCCGAAATGTATCATCTTC 1249
QY 1088 CCTATGCACTTATCTGTTGGCCTTTGTAGACATCGTGTCTTTTATTCAAAGTCCTAG 1147
Db 1250 CTATAGGTAGTCTAAACAATGGGCTTTTCCGGCATCGTGCCATCCTATTAAAGAAATTGG 1309
QY 1148 CTGATTCAATTGAATTAACCTGTTCGAATGCAAGGATGTAATAATTGCACTAGAGATG 1207
Db 1310 CTGATTACATAGGTTTACCATGTCCGATAGCTCGAGGTTGCAGATACTGTAAGAGAGCC 1369
QY 1208 ATGCTTCATCTGCTTGTAGGTTTCG-----GGGTTGATAGGGAATCTCA 1255
Db 1370 ACCAATCTTCTTGCTTGTCAAGATTGACGATGACAGGAAGCTTCAAGGGAATATGTAG 1429
QY 1256 TCGATCTGATTGGAGGCCAGGTTGCTTATGCAACCTGATTTCTTGTCAATGGTCCAT 1315
Db 1430 TTGACCTCATCGGGGAACAGGAATGTCCATGATCCGGATTCCTCTATCAACGGTGAAA 1489
QY 1316 CATCCATCTCAATTTCTCACCATTGCGATTTCCAAGACTAAAACCTATTGAATCTACCA 1375
Db 1490 CACAGTGTCAAGATTCCTTCACCTCTTCAATGAGTCACTCTTACAGATTTTCCAG---- 1544
QY 1376 TTGATTTCAAGTCACTGGCCAAACAGTATTTCTTGGATAGCCCAATCACTTAATCTGTAT 1435
Db 1545 -----GCCTTGGGTGCATAGTACATCTCCTTGTCAAGCTG 1579
QY 1436 TTGATGAAGCTTCTTCAGGTAATGTTGTATCTGGGAAGGATGCTGCATTTCTCGTCTATC 1495
Db 1580 TAGAGTCAAGACITTCACGCACTCTTTCTGAAAAACATTCACAGTTCAAGGAGTCAAGCC 1639
QY 1496 AAAGGCCATTAAATAGGAAGGATGTAGATGGAAAAACCATAGTGGTTACTGGTGACAAGG 1555
Db 1640 AAGTACACAAGAAATTTGAGTTGCTGATTAACGCGAGGACAGTATGTTGTCTCATATTG 1699
QY 1556 ACAGAAATTTCTCAGTTATTAAATAAAAAAGCAGCCCACTGAATACTCAAGATGGAAGT 1615
Db 1700 ATCAAACTTGCTGTGCAAAAGTATCATCAATGGTTTTGACAGAACTGTTCTTCGAGCTC 1759
QY 1616 CTGAGCAATTTAGATCATGTGTTGCTTCTCCATATAGTGTACAGTCGACCCCTTTTGTAG 1675
Db 1760 TACCACCTTGATATACCAAACTTAGTGAAGAAAAGATTGCCCCCAAGAAACCTGCAAG 1819
QY 1676 AAAATGTAGTCCCTTTAAGCCATATCTCACATATTGTTCTGAAGATTCGGAGCATCTCT 1735
Db 1820 AAGAAACCGTTCTATTAGAAGATCCAAACAGCTATGAAGCAGCCAAACTTATCAGTTGAC 1879
QY 1736 TAGCATGTCTCATCCAAGGATGGATCATGTTAAACAATTTACCATTTGTTCTCATGGTAGTC 1795

Db 1880 CAGAGATAGTAGGCTGACACTCGAAAAAGATAAAAAAGGAAGTTACCTGTTGACGCCA 1939
QY 1796 AGTTGATTAGAAAAACCAATAGAGCTTCCCTTGGCTTAGAAGATTTGGTTATTCCATGGA 1855
Db 1940 TCTCACCTTACTTGACTATTGAACCTTCTTTGGCATCAGATTGGCTGGAGGTTCTCATGGA 1999
QY 1856 CAGATCTTGATTTGAGGGAGAAAAATTGGAGCAGGTTCTTTGGGACTGTATATCTGTTG 1915
Db 2000 ATGAATTACATATCAAGAGCGTGTGGTGCTGGATCAATTGGAACCTGTTTCATCGTCTG 2059
QY 1916 AGTGGCATGGCTCTGATGTTGCTGTGAAGATCCTCAAGAACAGACTTCCATCTCTGAAC 1975
Db 2060 AGTGGCATGGATCAGATGTTGCTGTCAAGATTTTGTCTAATTCAAGATTTCCATGATGACC 2119
QY 1976 GTGTTAATGAGTTTCTGAGAGA-----GGTTGCTATCATGAAATCTTTAC 2020
Db 2120 AATTCAAGAAATTTCTCAGAGAGGTATGTAAAGCAAGCGGTTGCTATATGAACCGTGTTC 2179
QY 2021 GACATCCTAATATTGTACTGTTTATGGGTGCGGTGACCAAGCCACAAACTTGTGTCATTG 2080
Db 2180 GTCACCCAAATGTTTCTCTTCATGGGTGCTGTGACAGAGCGACCCCGTTTATCAATAA 2239
QY 2081 TCACCGAATATCTATCGAGAGGTAGCTGTATAGGCTTTTGCATAAAGTCAG---GTGTCA 2137
Db 2240 TAAACAGAATATTTCGCAAGAGGCGAGTCTTTTTCGCTTATCCATAGGCCAGCTTCTGGGG 2299
QY 2138 AAGACATAGATGAACACACGTGCAATAAATATGGCTTTTGTATGTG----- 2181
Db 2300 AGTTGCTAGATCAGAGAGGAGGCTACGTATGGCATTTGGATGTGGTTTGTGCTATTCCCC 2359
QY 2182 -----GCAAGGGAATGAACACTACCTCCACAGACAGTGTATCCTCCAAATTTGTATCGTGAT 2236
Db 2360 ATTATGCCAAGGCTCAACTACCTACACTGTCTTAATCCTCTCTGTAGTGCATTGGGACC 2419
QY 2237 TAAATCACCGAATCTGTGTAGTTGACAAAGATATACAGTCAAGGTTTGTGATTTTGGTC 2296
Db 2420 TGAATCTCCAAATCTACTGTTGATAAGAACTGGACAGTGAAGGTTTGCATTTTGGAC 2479
QY 2297 TCTCCCGTTTAAAGSCACGCACATTTCTTTCATCCAAATCTGCAGCTGGAACACCTGAAT 2356
Db 2480 TTTCAAGATTCAAGSCAAACACTTTTCATACCATCAAAATCTGTTGCAGGAACACCTGAGT 2539
QY 2357 GGATGGCACCAGAGTACTACGCGATGAACCATCAAAATGAAAGTCAAGATGTTTACAGCT 2416
Db 2540 GGATGGCTCCAGAGTTTCTTAGAGGGGAACCGACAAACGAGAAATCAGATGTTTACAGTT 2599
QY 2417 TTGAGTGATTTTGTGGAGTTGGCAACTTTGCAACAGCCATGGTGTATCTAAACCCAG 2476
Db 2600 TCGAGTAGTCTTATGGGAGTTGATTACTTTGCAACAGCCTTGGAATGGACTCAGTCTCTG 2659
QY 2477 CTCAGGTTGTGCGAGCTGTTGGATTTTAAGGGCAAAAGGCTTGACATCCACGATGTATA 2536
Db 2660 CTCAGGTGTTGGAGCAGTTGCATTTCCAGAACAGGCGGCTTATATTCCTCCCAACACCT 2719
QY 2537 ATCCAAATTTGGCTTCTTAATAGTGGCTTGTGGCCGATGAGCCATGGAACGTCCTT 2596
Db 2720 CTCGGTTTGGTATCTCTAATGGAAGCTTGTGCGCAGATGAGCCGTCTCAGCGGCCAG 2779
QY 2597 CTTTTTCCAGCATTTATGGAACCTTGAA 2624
Db 2780 CATTGGTAGTATAGTGGACACATTGAA 2807

RESULT 4
US-09-938-842A-1085
; Sequence 1085, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krebs, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong


```

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1085
; LENGTH: 2661
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-1085

Query Match          9.0%;   Score 296.4;   DB 10;   Length 2661;
Best Local Similarity 63.6%;   Pred. No. 4e-70;
Matches 469;   Conservative 0;   Mismatches 266;   Indels 3;   Gaps 1;

QY 1834 GAAGATTGGTTATTCCTGACAGATCTTGATTGAGGGAGAAAATTGGAGCAGGTTCT 1893
Db 1918 GCAAAGTGGGAATTATGTGGGAAGATCTTCAGATGGCGAGCGCATGGTATTGGTTCA 1977

QY 1894 TTTGGACTGTATATCGTGGTGAGTGGCATGGCTCTGATGTTGCTGTGAAGATCCTCACA 1953
Db 1978 TATGGAGAAGTTTATCGTGCAGAGTGAATGGAATGGAAGTGGCTGTGAAGATTTCTG 2037

QY 1954 GAACAAGACTTCCATCCTGAACGTGTTAATGAGTTTCTGAGAGAGGTTGCTATCATGAAA 2013
Db 2038 GACCAAGATTCTCTGTTGATGTCATGACACAGTTCAAAATCTGAAATTGAAATAATGTTG 2097

QY 2014 TCTTTACGACATCCTAATATTGACTGTTTATGGTGCGGTGACCAAGCCACCACAACTTG 2073
Db 2098 AGGTTACGGCATCCAAACGTTGTTCTTTTCATGGGAGCAGTTACTCGTCCCCCAAATTC 2157

QY 2074 TCCATTGTCACCGAATATCTATCGAGAGGTAGCTTGTATAGGCTTTTGCATAAGTCAGGT 2133
Db 2158 TCCATCCTGACAGAGTTCTTACCAGGGGAAGTTTGTATAGATTACTCCATCGGCC--G 2214

QY 2134 GTCAAAGACATAGATGAACACACGTCGAATAAATATGGCTTTTGTATGGCAAAGGGAATG 2193
Db 2215 AACCATCAGCTTGATGAGAAGAGGAGAATCGGATGGCTCTTGATGTGGCAAAGGGAATG 2274

QY 2194 AACTACCTCCACAGACGTGATCCTCCAATGTTTCATCGTGATTTTAAATCACCGAATCTG 2253
Db 2275 AACTACTTACACACCAGCCACCCGACTGTTGTACATAGGATTTAAATCTCCAAACCTT 2334

QY 2254 TTAGTTGACAAGAAGTATACAGTCAAGGTTTGTGATTTTGGTCTCTCCCGTTTAAAGGCA 2313
Db 2335 CTTGTTGATAAATAATGGGTTGTGAAGGTTTGTGATTTTGGATTGTCCCGCATGAACAC 2394

QY 2314 CGCACATTTCTTTTCATCCAAATCTGCAGCTGGAACACACCTGATGGATGGCACCAGAACTA 2373
Db 2395 CACACATATTTGTCCTCGAAATCAACTGCAGGAACGCCCTGAGTGGATGGCTCCAGAACTG 2454

QY 2374 CTACGGGATGAACCATCAAAATGAAAAGTCAGATGTTTACAGCTTTGGAGTGATTTGTGG 2433
Db 2455 TTGAGGAATGAACCCGGTAAATGAGAAATGTGACGTGTACAGCTTTGGTGTCAATATGTTG 2514

QY 2434 GAGTTGGCAACTTTTGAACAGCCATGGTGTAAATCTAAACCCAGCTCAGGTTGTCGAGCT 2493
Db 2515 GAATTAGCTACTTTCACCGCTCCCTTGGAAAGGTTTGAACCCCGATGCAAGTCGTTGGAGCT 2574

QY 2494 GTTGGATTTAAGGGCAAAAGGCTTGACATCCACAGTGATGTAAATCCCAATTTGGCTTCC 2553
Db 2575 GTGGGATTCAGAAATCGACGCCCTTGAAATCCAGATGATATCGATCTAACTGTGGCACAG 2634

QY 2554 TTAATAGTGGCTTGCTGG 2571
Db 2635 AATAATCCGTGAATGTTGG 2652
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RESULT 5
US-09-938-842A-1577
; Sequence 1577, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1577
; LENGTH: 2211
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-1577

Query Match          8.2%;   Score 270.2;   DB 10;   Length 2211;
Best Local Similarity 60.8%;   Pred. No. 5.5e-63;
Matches 459;   Conservative 0;   Mismatches 293;   Indels 3;   Gaps 1;

QY 1846 ATTCCATGGACAGATCTTGATTGAGGGAGAAAATTGGAGCAGGTTCTTTTGGACTGTA 1905
Db 1387 ATACGATGGGAAGATCTACAACCTGGGGAGGAGGTGCGAAGAGGTTTCATTTGCTGCGGTT 1446

QY 1906 TATCGTGGTGAGTGGCATGGCTCTGATGTTGCTGTGAAGATCCTCACAGAACAAAGACTTC 1965
Db 1447 CATCGTGGAGTTTGGAAATGGATCGGATGTTGCTATTAAAGGTTTACTTCGATGTGATTAC 1506

QY 1966 CATCCTGAACGTGTTAATGAGTTTCTGAGAGAGGTTGCTATCATGAAATCTTTACGACAT 2025
Db 1507 AATGCGATGACTTTGACGGAGTGCAGAAAAGGAGATCAACATTTATGAAGAAACTGAGACAT 1566

QY 2026 CCTAATATTGTTACTGTTTATGGTGGTGGTGACCAAGCCCAAACTTGTCATTGTCCACC 2085
Db 1567 CCGAATGTGCTACTATTATTATGGGAGCAGTATGTACAGAAAGAAAATCTGCCATAATCATG 1626

QY 2086 GAATATCTATCGAGAGGTAGCTTGTATAGGCTTTTGCATAAAGTCAGGTGTCAAAGACATA 2145
Db 1627 GAATATATGCCAAGAGGGAGTCTCTTCAAAATACTTTCATAATACGAAT--CAGCCATTG 1683

QY 2146 GATGAAACACGTCGAATAAATATGGCTTTTGTATGGCAAAGGGAATGAACCTACCTCCAC 2205
Db 1684 GACAAGAAACGCCGTTTAAGAATGGCCCTTGATGTTGCTAGGGGAATGAATTACTTACAC 1743

QY 2206 AGACGTGATCCTCCAATTGTTTCATCGTGATTTAAATCACCGAATCTGTTAGTTGACAAG 2265
Db 1744 CGCAGAAATCCGCCAATTGTACATAGAGACTTGAAATCTTCCAATCTACTCGTGGACAAG 1803

QY 2266 AAGTATACAGTCAAGGTTTGTGATTTTGGTCTCTCCCGTTTAAAGGCACGCACATTTCTT 2325
Db 1804 AACTGGAATGTCAAGTTGGAGACTTTGGGTTTATCAAAGTGAAGAACGCAACCTTCTTG 1863

QY 2326 TCATCCAAATCTGCAGCTGGAACACCTGATGGATGGCACCAGAGTACTACCGCATGAA 2385
Db 1864 AGTACTAAATCCGGGAAAGGAACCTCCGCAAGTGATGGCTCCTGAAAGTTCTCAGAAGTGAA 1923

QY 2386 CCATCAAATGAAAAGTCAGATGTTTACAGCTTTGGAGTGATTTTGTGGAGTTGGCAACT 2445
Db 1924 CTTTCGAATGAGAAAGTGTGATGTTTCAGCTTTGGAGTCATCTTATGGGAGCTAATGACT 1983
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Db 909 TCTCAAGCCTGAGCGTGTAAATGCGGAATGCTACGAGAGTCTTCTCAGGAAGTATATAT 968
QY 2007 CATGAATCTTTACGACATCTTAATATTGACTGTTTATGGTGGGTGACCAAGCCACC 2066
Db 969 AATGAGGAAGTTCGGCATAAAATGTTGTCAGTTTCATTGGTGCATGTACAGCATCACC 1028
QY 2067 AAACCTGTCCATTGTACCGGAATATCTATCGAGAGGTAGCTTGTATAGGCTTTTGCATAA 2126
Db 1029 AAACCTGTCCATTGTGACAGAGTTTCAATCTCGGGGAGCAATTTATGATTTCTCTTCAAA 1088
QY 2127 GTCAGGTGTCAAAGACATAGATGAACACGTCGAATAAATATGGCTTTTGTATGGCAAA 2186
Db 1089 ACACAAAGGGGTTTTTAAATTCATC---TTTGCTCAAAGTGGCACTCGACGTCGAA 1145
QY 2187 GGGATGAACCTACCTCCACAGAGGTGATCTCCCAATTGTTCACTGATTTAAATCACC 2246
Db 1146 AGGAATGAATATCTGCAATCAAAAT-----ATTATTCATAGAGACCTTAAGACTGC 1199
QY 2247 GAATCTGTAGTTGACAAAGATATACAGTCAAGGTTTGTGATTTGGTCTCTCCGCTTT 2306
Db 1200 TAATCTCTTATGGACGAACATGAAGTTGCAAGTTGCCGATTTGGTGTGCGAGAGT 1259
QY 2307 AAAGCAGGCACATTTCTTTCATCCAAATCTGACGCTGGAAACACCTGAATGGATGGCACC 2366
Db 1260 GCAGACTGAGTCAGGGT---ATGACAGCGGAACAGGACATACCGATGGATGGCTCC 1316
QY 2367 AGAAGTACTACGGATGAACCATCAATGAAAGTCAAGTGTGATTTTACAGCTTTGGAGTGAT 2426
Db 1317 AGAGGTCAATTGACCAACAACTTATGATCAAGGGCAGATGCTTCACTACCGCATGAT 1376
QY 2427 TTTGTGGAGTTGGCAACTTTGCAACAGCCATGGTGTAAATCTAAACCCAGCTCAGTTGT 2486
Db 1377 GCTGTGGAACTTTTGACTGGGAACTCCCATATTTCTTACTTGACTCCACTGCAAGCTGC 1436
QY 2487 CGCAGCTGTTGATTTAAGGCAAAAGGCTTGACATCCACCGTGTAAATCCCAAATT 2546
Db 1437 TGTGGGTTGTTCCAAAGGACTTAGACCAAAATTTCCAAAGGAACACACCCCAAACT 1496
QY 2547 GGCCTTCTTAATAGTGGCTTGTGGCGGATGAGCCATGGAACGTCCTTCTTTTCCAG 2606
Db 1497 GACTGACTTCTTGAGAAATGCTGGCAGCAAGACCCAGCTCTAAGACCCCAATTTTGCAGA 1556
QY 2607 CATTATGAAACCTTGAACCAATGA 2632
Db 1557 AATCATAGAAATGCTTAACCAACTAA 1582

RESULT 9
US-09-938-842A-903
; Sequence 903, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCSIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 903
; LENGTH: 1638
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-903

Query Match 3.4%; Score 111.8; DB 10; Length 1638;
Best Local Similarity 54.3%; Pred. No. 1.4e-19;
Matches 296; Conservative 0; Mismatches 237; Indels 12; Gaps 3;
QY 1906 TATCGTGTGAGTGGCATGCTCTGATGTTGCTGTGAAGATCCTCAGAGAACAGACTTC 1965
Db 877 TATAAGGTACATACCTGTAGCCAGGAAGTTGCTATCAAGTCTTAAAGCCAGAGCGTCTA 936
QY 1966 CATCCTGAACGTTGTTAATGAGTTTCTGAGAGAGGTTGCTATCATGAATCTTTACGACAT 2025
Db 937 GACTCAGATCTAGAGAAAGAGTTTGCCCAAGAGTCTTTTATTATGAGAAAGTTAGACAC 996
QY 2026 CCTAATATGTTACTGTTTATGGTGGTGGTGGACCAAGCCACCAAACTTGTCCATTGTCCACC 2085
Db 997 AAAAATGTTGTTCAAGTTCAATGGTCTTGCCCAAGCCCTCCACATCTGTGTATCGTTACA 1056
QY 2086 GAATATCTATCGAGAGGTAGCTTGTATAGGCTTTTGCATAAGTCAAGTGTCAAAGACATA 2145
Db 1057 GAATTCATGCCCGGTGGAAGTGTATATGACTATACACAAGCAAAAGGGC--GTCTTT 1113
QY 2146 GATGAACACGTCGAATAAATATGCTTTTGTGTTGGCAAGGGAATGAACCTACCTCCAC 2205
Db 1114 AAGCTTCCAACTTTGTTTAAAGTAGCTATAGATATTGCAAGGGATGAGCTACTTACAC 1173
QY 2206 AGACGTGATCCTCCAATTTGTTTCATGCTGATTTAAATCAACCGAATCTGTAGTTGACAAG 2265
Db 1174 CAAAATAA-----CATAAATTCACAGAGATTTGGAAGGCTGCCAACCTCTTAATGGACGAA 1227
QY 2266 AAGTATACAGTCAAGGTTTGTGATTTTGGTCTCTCCCGTTTAAAGGCACGCACATTTCCT 2325
Db 1228 AATGAGGTGTTAAGGTTGCAAGCTTTGGGCTGGCTAGAGTGAAGCACAACAACTGGAGTT 1287
QY 2326 TCATCCAAATCTGCAGCTGGAAACACCTGAATGGATGGCACCAGAGTACTACGCGATGA 2385
Db 1288 ---ATGACAGCTGAAACTGGAACATATCGCTGGATGGCTCCAGAGGTGATAGAACAACAAAG 1344
QY 2386 CCATCAAAATGAAAGTCAAGTGTGATGTTTACAGCTTTGAGTGAATTTGTGGAGTTGGCAACT 2445
Db 1345 CCATATGATCACAAGGCTGACGTATTTCAGTACGGGATTTGTCTATGGGAGTTGTTGACT 1404
QY 2446 TTGCA 2450
Db 1405 GGGAA 1409

RESULT 10
US-09-923-876-1947
; Sequence 1947, Application US/09923876
; Patent No. US20020013958A1
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 1947
; LENGTH: 246
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700159794H1
US-09-923-876-1947

	Query Match	2.6%;	Score 84.8;	DB 9;	Length 246;
	Best Local Similarity	62.4%;	Pred. No. 1.1e-12;		
	Matches 151;	Conservative	0;	Mismatches 87;	Indels 4;
					Gaps 1;
QY	2065	CCAAACTTGTCCATTGTCACCGAATATCTATCGAGAGGTAGCTGTATAGGCTTTTGCAT	2124		
Db	9	CCTCATCTTTCTATCGTGACTGAATTTCTGCCAAGGGTAGTTTATTTTCGGTTAATCCAT	68		
QY	2125	AAGTCAGGTGTCAAAGACATAGATGAAACACGTCGAATAAATATGGCTTTTGATGTGGCA	2184		
Db	69	AGGCCCAAT---AACCAGTTGGATCAAAAAGGCGTTTAAGGATGGCACTTTGATGTGGCA	124		
QY	2185	AAGGGAATGAACTACTCCACAGACGTGATCCTCCAATTGTTTCATCGTGATTTAAATCA	2244		
Db	125	CGTGGTATGAATTATTACACAATTGCAACCCAGTCATAGTTCACCGAGACTTGAAATCT	184		
QY	2245	CCGAATCTGTTAGTTGACAAGAAGTATACAGTCAAGGTTTGTGATTTTGGTCTCTCCCGT	2304		
Db	185	CCAAATCTACTTTGTTGACAAAAATTGGGTTGTGAAGGCTCTGTGATTTTGGTTTATCACGT	244		
QY	2305	TT	2306		
Db	245	CT	246		

RESULT 11
 US-10-106-698-2068/c
 ; Sequence 2068, Application US/10106698
 ; Publication No. US20030109690A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
 ; FILE REFERENCE: PA005P1
 ; CURRENT APPLICATION NUMBER: US/10/106,698
 ; CURRENT FILING DATE: 2002-03-27
 ; PRIOR APPLICATION NUMBER: PCT/US00/26524
 ; PRIOR FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: US 60/157,137
 ; PRIOR FILING DATE: 1999-09-29
 ; PRIOR APPLICATION NUMBER: US 60/163,280
 ; PRIOR FILING DATE: 1999-11-03
 ; NUMBER OF SEQ ID NOS: 8564
 ; SOFTWARE: PatentIn Ver. 3.0
 ; SEQ ID NO 2068
 ; LENGTH: 1063
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-106-698-2068

Query Match	2.6%;	Score 84.2;	DB 14;	Length 1063;	
Best Local Similarity	47.3%;	Pred. No. 4.1e-12;			
Matches 325;	Conservative	0;	Mismatches 353;	Indels 9;	Gaps 2;
QY	1992	GAGAGAGGTTGCTATCATGAAATCTTTACGACATCCTPAATATTGTACTGTTTATGGGTGC	2051		
DB	741	GAAGAGGCAGAAATACTCAGTGTCTCAGTCACAGAAACATCATCCAGTTTTATGGAGT	682		
QY	2052	GGTGACCAAGCCACCAACTGTCTCCATTGTTCACCGAATATCTATCGAGAGGTAGCTTGTA	2111		
DB	681	AATTCTTGAACCTCCCACTATGGCATTTGTCACAGAAATATGCTTCTCTGGGATCACTCTA	622		
QY	2112	TAGGCTTTTGCATAAGTCAGGTGTCAAAGACATAGATGAAACACGTCGAATAAATATGGC	2171		
DB	621	TGATTACATTAACAGTAACAGAAAGTGAGGAGATGGATATGGATCACATTATGACCTGGGC	562		
QY	2172	TTTTGTATGTGGCAAAGGGAATGAACTACCTCCACAGACGTGATCCTCCAATTG---TTCA	2228		
DB	561	CAC TGATGTAGCCAAAGGAATGCATTATTTACATATGGAGGCTCCTGTCAAGGTGATCA	502		
QY	2229	TCGTGATTTAAAAATCACCGAATCTGTTAGTTGACAAGAAAGTATACAGTCAAGGTTTGTGA	2288		
DB	501	CAGAGACCTCAAGTCAAGAAACGTTGTTATAGCTGTCTGATGGAGTATTGAAGATCTGTGA	442		

Qy	2289	TTTGGTCTCTCCCGTTTAAAGCAGCACATTCTTTTCATCCAAATCTGCAGCTGGAAC	2345
Db	441	CTTTGGTGCCTCTCGGTTCCATAACCATACAA-----CACACATGTCCTTGGTTGGAAC	388
Qy	2349	ACCTGAATGGATGGCCACCAGAAAGTACTACGGGATGAACCATCAAAATGAAAAGTCAGATGT	2408
Db	387	TTTCCCATGGATGGCTCCAGAAAGTTATCCAGAGTCTCCCTGTGTGTCAGAAACTTGTGACAC	328
Qy	2409	TTACAGCTTTGGAGTGATTTTGTGGGAGTTGGCAACTTTTGCAACAGCCATGGTGTAAATCT	2468
Db	327	ATATTCTATGGTGTGGTTCTCTGGGAGATGCTAACAAAGGGAGGTCCCTTTAAAGGTTT	268
Qy	2469	AAACCCAGCTCAGGTTGTGCGCAGCTGTTGGATTTAAGGGCAAAAGGCTTGACATCCCAAG	2528
Db	267	GGAGGATTACAAGTAGCTTGGCTTGTAGTGGAAAAAACAAGAGAGATTAAACCATCCCAAG	208
Qy	2529	TGATTAATAATCCCAAATTTGGCTTCTTAATAGTGGCTTGCTGGCGGATGAGCCATGGAA	2588
Db	207	CAGTTGCCCCAGAAAGTTTGTCTGAACTGTTACATCAGTGTGGGAAGCTGATGCCAAGAA	148
Qy	2589	ACGTCCTTCTTTTCCAGCATTATGGAAACCTTGAAACCAATGACTAAACAAGCGCCACC	2648
Db	147	ACGGCCATCATTCAGCAAAATCATTTCAATCCTGGAGTCCATGTCAAATGACACGAGCCT	88
Qy	2649	TCAACAAAAGTCGCACAGACACCCCTCTC	2675
Db	87	TCTGACAAGTGTAACCTCATTTCCCTACAC	61

RESULT 12
 US-09-757-982-6
 ; Sequence 6, Application US/09757982
 ; Patent No. US20020094559A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Acton, Susan
 ; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
 ; FILE REFERENCE: MNI-050
 ; CURRENT APPLICATION NUMBER: US/09/757,982
 ; CURRENT FILING DATE: 2001-01-10
 ; PRIOR APPLICATION NUMBER: 09/163,115
 ; PRIOR FILING DATE: 1998-09-29
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 6
 ; LENGTH: 1365
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1365)
 US-09-757-982-6

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RESULT 12
US-09-757-982-6
; Sequence 6, Application US/09757982
; Patent No. US20020094559A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/757,982
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 09/163,115
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
US-09-757-982-6

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	Query Match 2.5%;	Score 81.6;	DB 9;	Length 1365;
	Best Local Similarity 47.4%;	Pred. No. 2.5e-11;		
	Matches 314;	Conservative 0;	Mismatches 339;	Indels 9; Gaps 2;
QY	1992	GRGAGAGTTGCTATCATGAATCTTTACGACATCCTAATATTGTACTGTTTATGGGTGC	2051	
Db	153	GAAAGAGGCAGAAATACTCAGTGTCTCAGTCACAGAAACATCATCCAGTTTTATGGAGT	212	
QY	2052	GGTGACCAAGCCACCAAACTTGTCCATTGTCACCGAATATCTATCGAGAGGTAGCTTGTA	2111	
Db	213	AAATCTTTGAACCTCCCAACTATGGCATTGTCAAGAATATGCTTCTCTGGGATCACTCTA	272	
QY	2112	TAGGCTTTTGCATAAGTCAGGTGTCAAAGACATAGATGAAACACGTCGAATAAATATGGC	2171	
Db	273	TGATTACATTAAACAGTAACAGAAAGTGAGGAGATGGATATGGATCACATTATGACCTGGGC	332	
QY	2172	TTTTTGATGTGGCAAAGGGAATGAACTACCTCCACAGACGTGATCCTCCAATTG--TTCA	2228	
Db	333	CAC TGATGTAGCCAAAGGAATGCATTATTTTACATATGGAGGCTCCTGTCAAGGTGATTCA	392	
QY	2229	TCGTGATNTAAAATCAACCGAATCTGTTAGTTGACAAGAAGTATACAGTCAAGGTTTGTGA	2288	

Db 393 CAGAGACCTCAAGTCAAGAAACGTTGTTATAGCTGCTGATGGAGTACTGAAGATCTGTGA 452
QY 2289 TTTTGGTCTCTCCCGTTTAAAGGCACGCACATTTCTTTTCATCCAAATCTGCAGCTGGAAAC 2348
Db 453 CTTTGGTGCCCTCGGTTCCATAACCATACA-----ACACACATGTCTCTGGTTGGAAAC 506
QY 2349 ACCTGAATGGATGGCACCAGAAAGTACTACGCGATGAACCATCAAATGAAAAGTCAGATGT 2408
Db 507 TTTCCCATGGATGGCTCCAGAAAGTTATCCAGAGTCTCCCTGTGTTCAGAAACTTGTGACAC 566
QY 2409 TTACAGCTTTGGAGTGATTTTGTGGGAGTTGGCAAACCTTTGCAACAGCCATGGTGTAAATCT 2468
Db 567 ATATTCCATGTGTGGTTCTCTCTGGGAGATGCTAAACAAGGGAGGTCCCTTTAAAGGTTT 626
QY 2469 AAACCCAGCTCAGGTTGTGCGAGCTGTGGATTTAAGGGCAAAAGGCTTGACATCCCACG 2528
Db 627 GGAAGGATTACAAGTAGCTTGGCTTGTAGTGGAAAAAACCAGAGATTAAACCATTCCAAG 686
QY 2529 TGATGTAAATCCCAAATTGGCTTCCTTAATAGTGGCTTGTGGCCGATGAGCCATGGAA 2588
Db 687 CAGTTGCCCCAGAAAGTTTGTCTGTAAGTGTACATCAGTGTGGGAAGCTGATGCCAAGAA 746
QY 2589 AGTCTCTCTTTTCCAGCATTATGGAACCTTGAAACCAATGACTAAACAGAGCCAC 2648
Db 747 ACGGCCATCATCAAGCAAATCATTTCAATCCTGGAGTCCATGTCAAAATGACACGAGCCT 806
QY 2649 TC 2650
Db 807 TC 808

RESULT 13
US-09-757-982-4
; Sequence 4, Application US/09757982
; Patent No. US20020094559A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/757,982
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 09/163,115
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2120
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (47)..(1411)
US-09-757-982-4

Query Match 2.5%; Score 81.6; DB 9; Length 2120;
Best Local Similarity 47.4%; Pred. No. 3.4e-11;
Matches 314; Conservative 0; Mismatches 339; Indels 9; Gaps 2;
QY 1992 GAGAGAGGTTGCTATCATGAAATCTTTACGACATCCTAATATTGTACTGTTTATGGGTGC 2051
Db 199 GAAAGAGGCAGAAATACTCAGTGTCTCCTCAGTCACAGAAACATCATCCAGTTTATGGAGT 258
QY 2052 GGTGACCAAGCCACCAAACTTGTCCATTGTCCCGAATATCTATCGAGAGGTAGCTTGTA 2111
Db 259 AATTCTTGAACCTCCCAACTATGGCATTGTTCACAGAATATGCTTCTCTGGGATCACTCTA 318
QY 2112 TAGGCTTTTGCATAAGTCAGGTGTCAAGACATAGATGAACACGTCGAATAAATATGCG 2171
Db 319 TGATTACATTAAACAGTAACAGAAAGTGAGGAGATGGATATGGATCATCATTTATGACCTGGC 378
QY 2172 TTTTGATGTGGCAAGGGAATGAACCTACCTCCACAGACGTGATCCTCCAATTG--TTCA 2228

Db 379 CACTGATGTAGCCAAAGGAATGCATTATTTACATATGGAGGCTCCTGTCAAGGTGATTCA 438
QY 2229 TCGTGATTTAAATCACCGAATCTGTTAGTTGACAAGAACTATACAGTCAAGGTTTGTGA 2288
Db 439 CAGAGACCTCAAGTCAAGAAACGTTGTTATAGCTGCTGATGGAGTACTGAAGATCTGTGA 498
QY 2289 TTTTGGTCTCTCCCGTTTAAAGGCACGCACATTTCTTTTCATCCAAATCTGCAGCTGGAAC 2348
Db 499 CTTTGGTGCCCTCTCGGTTCCATAACCATACA-----ACACACATGTCTCTGGTTGGAAAC 552
QY 2349 ACCTGAATGGATGGCACCAGAAAGTACTACGCGATGAACCATCAAATGAAAAGTCAGATGT 2408
Db 553 TTTCCCATGGATGGCTCCAGAAAGTTATCCAGAGTCTCCCTGTGTTCAGAAACTTGTGACAC 612
QY 2409 TTACAGCTTTGGAGTGATTTTGTGGGAGTTGGCAAACCTTTGCAACAGCCATGGTGTAAATCT 2468
Db 613 ATATTCCATGTGTGGTTCTCTCTGGGAGATGCTAACAAAGGAGGTCCCTTTTAAAGGTTT 672
QY 2469 AAACCCAGCTCAGGTTGTGCGAGCTGTGGATTTAAGGGCAAAAGGCTTGACATCCCACG 2528
Db 673 GGAAGGATTACAAGTAGCTTGGCTTGTAGTGGAAAAAACCAGAGATTAAACCATTCCAAG 732
QY 2529 TGATGTAAATCCCAAATTGGCTTCCTTAATAGTGGCTTGTGGCCGATGAGCCATGGAA 2588
Db 733 CAGTTGCCCCAGAAAGTTTGTCTGTAAGTGTACATCAGTGTGGGAAGCTGATGCCAAGAA 792
QY 2589 ACGTCTCTCTTTTCCAGCATTATGGAACCTTGAAACCAATGACTAAACAGCGCCACC 2648
Db 793 ACGGCCATCATCAAGCAAATCATTTCAATCCTGGAGTCCATGTCAAATGACACGAGCCT 852
QY 2649 TC 2650
Db 853 TC 854

RESULT 14
US-09-770-444-370/c
; Sequence 370, Application US/09770444
; Patent No. US20020023280A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickler, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2027 (PARA-016PRV)
; CURRENT APPLICATION NUMBER: US/09/770,444
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,502
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 370
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:

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; NAME/KEY: misc_feature
; LOCATION: (1)...(463)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-444-370

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	Query Match	2.3%;	Score 74.8;	DB 9;	Length 463;
	Best Local Similarity	57.8%;	Pred. No. 9.1e-10;		
	Matches 133;	Conservative 0;	Mismatches 97;	Indels 0;	Gaps 0;
QY	2296	CTCTCCCGTTTAAAGGCACGCAATTTCTTTTCATCCAAATCTGCAGCTGGAAACACTTGAA	2355		
Dd	463	CTGTGAGAAATAATGACAGGGACAACAATGACAGACACAGTCTCTGCAGGAACCTCCAGAG	404		
QY	2356	TGSATGCCACCAGAAGTACTACGCGATGAACCATCAAATGAAAAGTCAGATGTTTACAGC	2415		
Dd	403	TGSATGGCTCCTGAACTTATCCGCAATGAGCCCTTCTCAGAAAAAGTGTATATCTTCAGT	344		
QY	2416	TTTGGAGTGATTTTGTGGGAGTTGGCAACTTTGCAACAGCCATGGTGTATCTAAACCCA	2475		
Dd	343	TTAGGTGTAATAATGTGGAGCTATGCACCTTTAACAGACCTTGGGAAGGAGTACCGCCT	284		
QY	2476	GCTCAGGTTGTCGAGCTGTTGGATTTAAGGGCAAAAGGCTTGACATCCC	2525		
Dd	283	GAACGGTGTGTTATGCTAATGCTTACGAGGAGCTCGGCTTGAGATTCC	234		

RESULT 15

US-10-440-341-2
; Sequence 2, Application US/10440341
; Publication No. US20030181413A1
; GENERAL INFORMATION:
; APPLICANT: RAPP, ULF
; APP, HARALD
; STORM, STEPHEN M.
; TITLE OF INVENTION: RAF PROTEIN KINASE THERAPEUTICS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVE., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/440,341
FILING DATE: 15-May-2003
CLASSIFICATION: <Unknown>

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PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/748,931
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: SCOTT, WATSON T.
 REGISTRATION NUMBER: 26,581
 REFERENCE/DOCKET NUMBER: 5683/82731
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-861-3067
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
SEQUENCE CHARACTERISTICS:
LENGTH: 2975 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 2
US-10-440-341-2

	Query Match	2.2%; Score 72.6; DB 12; Length 2975;
	Best Local Similarity	53.4%; Pred. No. 1.3e-08;
	Matches 325; Conservative	0; Mismatches 254; Indels 30; Gaps 7;
QY	1879 ATTGGAGCAGGTTCTTTTGGGACTGTATATCGTGGTGAGTGGCATGGCTCTGATGTTGCT	1938
Dd	1190 ATTGGGTGAGGCTCTTTTGGAACTGTTTTATAAGGGTAATGGCACGG--AGATGTTGCA	1246
QY	1939 GTGAAGATCCTCACAGAACAAAGACATTCCATCCTGAAACGTGTTAATCAGTTTCTGAGAGAG	1998
Dd	1247 GTAAAGATCCTAAAGTTGTGCAGCCCAAACCCAGAGCAATTCCAGGCCCTTCAGGAATGAG	1306
QY	1999 GTTGTATCATGAAATCTTTACGACATCCTAATATTGTACTGTGTTATGGGTGCGGTGACC	2058
Dd	1307 GTGGTGTCTGCGCAAAACACGGCATGTGAACATTCTGCTTTTTCATGGGTACATGACA	1366
QY	2059 AAGCCACCAAACTTGTCCATTGTACCGAATATCTATCGAGAGGTAGCTGTATAGGCTT	2118
Dd	1367 AAG---GACAACCTGGCAATTGTGACCCAGTGGTGGAGGGCAGCAGCCTCTACAAAAC	1423
QY	2119 TTGCATAAGTCAGGTGTCAAAGACATAGATGAAACACAGTCGAATAAATATGGCTTTTGAT	2178
Dd	1424 CTGCAT-GTCCAGGAGACCAAGTTTCAGATGTTCCA--GCTAATTGACATGCCCCGCGCAG	1480
QY	2179 GTGSCAAGGGAATGAACACTACCTCCACAGACGTGATCCTCCAATTGTTTCATCGTGATTTA	2238
Dd	1481 ACGGCTCAGGAATGGACTATTGCA----TGCAAAGAACATCATCCATAGAGACATG	1534
QY	2239 AAATCACCGAATCTGTTAGTTGACAAGBAGTATACAGTCAAGGTTTGTGATTTTGGTCTC	2298
Dd	1535 AAATCCAACAATATATTTCTCCATGAAGSCTTAACAGTGAAAAATTGGAGATTTTGGTTTG	1594
QY	2299 TCCCGTTTAAAGGCACGCACATTTCTTTTCATCCAAATCTG-----CAGCTGGAACACCT	2352
Dd	1595 GCAACAGTAAAGTCACGCTGGAGTGGTTCTCAGCAGGTTGAACAACCTACTGCTCTGTC	1654
QY	2353 GAATGGATGGCACCAGAAAGTACTACG-----CGATGAACCATCAATGAAAAAGTCA	2403
Dd	1655 CTC TGATGGCCCCAGAGGTGATCCGAATGCAGGATAACAACCCATTTCAGTTCCAGTCG	1714
QY	2404 GATGTTTACAGCTTTGGAGTGATTTTGTGGGAGTTGGCAACTTTGCAACAGCCATGGTGT	2463
Dd	1715 GATGTCTACTCCTATGGCATCGTATTGTATGAACCTGATGACGGGGGAGCTTCTTATTTCT	1774
QY	2464 AATCTAAAC	2472
Dd	1775 CACATCAAC	1783

Search completed: October 24, 2003, 08:16:51
Job time : 844 secs